```
                GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on:       April 21, 2006, 13:11:04 ; Search time 26 Seconds
                                          (without alignments)
                              529.727 Million cell updates/sec

Title:        US-10-664-421-1
Perfect score: 1670
Sequence:     1 MLLSKINSLAHLRAAPCNDL.........LLPQETAEIHLHSLSPGPSK 313

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched:     225428 seqs, 44002918 residues

Total number of hits satisfying chosen parameters:    225428

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :    Published_Applications_AA_New:*
         1: /SIDS7/ptcodata/1/pubpaa/US08_NEW_PUB.pep:*
         2: /SIDS5/ptcodata/1/pubpaa/US06_NEW_PUB.pep:*
         3: /SIDS5/ptcodata/1/pubpaa/US07_NEW_PUB.pep:*
         4: /SIDS5/ptcodata/1/pubpaa/PCT_NEW_PUB.pep:*
         5: /SIDS5/ptcodata/1/pubpaa/US09_NEW_PUB.pep:*
         6: /SIDS5/ptcodata/1/pubpaa/US10_NEW_PUB.pep:*
         7: /SIDS5/ptcodata/1/pubpaa/US11_NEW_PUB.pep:*
         8: /SIDS5/ptcodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	869.5	52.1	311	7	US-11-103-065-2	Sequence 2, Appli
2	384.5	23.0	256	6	US-10-507-346-74	Sequence 74, Appl
3	376	22.5	950	6	US-10-501-035-357	Sequence 357, App
4	368.5	22.1	631	7	US-11-241-056-11	Sequence 11, Appl
5	366	21.9	504	7	US-11-087-099-9816	Sequence 9816, Ap
6	364.5	21.8	256	6	US-10-877-346-72	Sequence 72, Appl
7	364.5	21.8	256	7	US-11-113-424-183	Sequence 183, App
8	356	21.3	514	7	US-11-087-099-11500	Sequence 11500, A
9	352	21.1	512	7	US-11-087-099-3997	Sequence 3997, Ap
10	352	21.1	514	7	US-11-087-099-3612	Sequence 3612, Ap
11	348.5	20.9	619	7	US-11-087-099-12402	Sequence 12402, A
12	348	20.8	472	7	US-11-087-099-11838	Sequence 11838, A
13	342.5	20.5	651	6	US-10-770-726-67	Sequence 67, Appl
14	342.5	20.5	651	7	US-11-177-138-10	Sequence 10, Appl
15	342	20.5	464	7	US-11-096-568A-22124	Sequence 22124, A
16	341	20.4	513	7	US-11-087-099-11726	Sequence 11726, A
17	340	20.4	620	7	US-11-087-099-3898	Sequence 3898, A
18	339.5	20.3	504	7	US-11-087-099-12331	Sequence 12331, A
19	339	20.3	713	6	US-10-995-561-881	Sequence 881, App
20	339	20.3	729	7	US-10-995-561-878	Sequence 878, App
21	339	20.3	737	6	US-10-995-561-880	Sequence 880, App
22	339	20.3	744	6	US-10-995-561-876	Sequence 876, App
23	339	20.3	753	6	US-10-995-561-877	Sequence 877, Appl
24	337.5	20.2	689	6	US-10-204-639-17	Sequence 17, Appl
25	336.5	20.1	445	7	US-11-096-568A-32575	Sequence 32575, A
26	336.5	20.1	448	7	US-11-096-568A-18364	Sequence 18364, A
27	333.5	20.0	1518	7	US-11-087-099-1886	Sequence 1886, Ap
28	332	19.9	439	7	US-11-096-568A-20431	Sequence 20431, A
29	332	19.9	443	7	US-11-096-568A-20430	Sequence 20430, A
30	328.5	19.7	715	6	US-10-204-639-65	Sequence 65, Appl
31	328	19.6	277	7	US-11-151-601-4	Sequence 4, Appli
32	327	19.6	358	6	US-10-979-095-6	Sequence 6, Appli
33	327	19.6	582	7	US-11-096-568A-32895	Sequence 32895, A
34	326.5	19.6	765	7	US-11-087-099-905	Sequence 905, App
35	325.5	19.5	278	6	US-10-055-877-149	Sequence 149, Appl
36	325.5	19.5	278	7	US-11-103-065-4	Sequence 4, Appli
37	325.5	19.5	278	7	US-11-151-601-10	Sequence 10, Appl
38	325.5	19.5	339	7	US-11-172-740-987	Sequence 987, App
39	324	19.4	401	7	US-11-087-099-6642	Sequence 6642, Ap
40	323	19.3	473	7	US-11-087-099-8865	Sequence 8865, Ap
41	323	19.3	513	7	US-11-087-099-7631	Sequence 7631, Ap
42	323	19.3	876	7	US-11-087-099-10193	Sequence 10193, A
43	322.5	19.3	611	7	US-11-087-099-8358	Sequence 8358, Ap
44	321.5	19.3	602	7	US-11-087-099-11542	Sequence 11542, A
45	319.5	19.1	432	7	US-11-096-568A-32576	Sequence 32576, A

ALIGNMENTS

```
RESULT 1
US-11-103-065-2
; Sequence 2, Application US/1110365
; Publication No. US20050282189A1
; GENERAL INFORMATION:
;  APPLICANT: Meyers, Rachel E., Lora, Jose M.
;  TITLE OF INVENTION: 2150, Human Protein Kinase Family
;  TITLE OF INVENTION: Member and Uses Therefor
;  FILE REFERENCE: MPI2001-137P1RNM
;  CURRENT APPLICATION NUMBER: US/11/103,065
;  CURRENT FILING DATE: 2005-04-11
;  PRIOR APPLICATION NUMBER: US/10/184,563
;  PRIOR FILING DATE: 2002-06-27
;  PRIOR APPLICATION NUMBER: 60/301,702
;  PRIOR FILING DATE: 2001-06-28
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;  LENGTH: 311
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-11-103-065-2

Query Match             52.1%;   Score 869.5; DB 7;  Length 311;
Best Local Similarity   58.4%;   Pred. No. 6.9e-72;
Matches  167;  Conservative  39;  Mismatches  75;  Indels  5;  Gaps  2;

Qy         28 GKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSDNLPVAIKHVEKDRISDWGELPNGTRVP 87
              |||:|::||:||||||||:|||||:|:||::||:::|||:::|:::::|:|::|||||||
Db         22 GKDREAFEAEYRLGPLLGKGGFGTVFAGHRLTDRLQVAIKVIPRNRVLGWSPLSDSVTCP 81

Qy         88 MEVVLLKKVSS--GFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELAR 145
              :|:|||:|:    |:||:||||||||:::|::|:|||||||:|||||:|||:|::|:|||:: 
Db         82 LEVALLWKVGAGGGHPGVIRLLDWFETQEGFMLVLERPLPAQDLFDYITEKGPLGEGPSR 141

Qy        146 SFFWQYLEAVRHCHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVYTDFDGTR 205
              .||:|::||:::|||:||:|||||||||||||:|||::|||||||||||:|::||||||||
Db        142 CFFGQVVAAIQHCHSRGVVHRDIKDENILIDLRRGCAKLIDFGSGALLHDEPYTDFDGTR 201

Qy        206 VYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDIPFEHDEIIRGQVFFRQRVSSECQH 265
              |||||||:|:|:||:|::|:||||||||||||||||||::|:||:|:|::|::|||::  
Db        202 VYSPPEWISRHQYHALPATVWSLGILLYDMVCGDIPFERDQEILEAELHFPAHVSPDCCA 261

Qy        266 LIRWCLALRPSDRPTPEEIQNHPWMQDVLLPQETAEIHLHSLSPGP 311
              |||.||| :.:||.:::::|:||||||.::   .:::|||::.||||
Db        262 LIRRCLAPKFSSRPSLEEILLDPWMQ---TPAEDVPLNPSKGGPAP 304
```

RESULT 2
US-10-877-346-74
; Sequence 74, Application US/10877346
; Publication No. US2006014153A1
; GENERAL INFORMATION:
; APPLICANT: Gerlach, Valerie L
; APPLICANT: MacDougall, John R
; APPLICANT: Smithson, Glennda
; APPLICANT: Millet, Isabelle
; APPLICANT: Stone, David
; APPLICANT: Gunther, Erik
; APPLICANT: Ellerman, Karen
; APPLICANT: Grosse, William M
; APPLICANT: Alsobrook II, John P
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine E
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Leach, Martin D
; APPLICANT: Shimkets, Richard A
; TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-124
; CURRENT APPLICATION NUMBER: US/10/877,346
; CURRENT FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US/09/964,956
; PRIOR APPLICATION NUMBER: 2001-09-26
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/235,631
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/235,633
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/235,808
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,064
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,065
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,066
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,135
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 60/237,434
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/238,321
; PRIOR FILING DATE: 2000-10-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 74
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Protein kinase
; OTHER INFORMATION: domain Consensus Sequence
US-10-877-346-74

Query Match   23.0%; Score 384.5; DB 6; Length 256;
Best Local Similarity   37.0%; Pred. No. 1.3e-27;
Matches   98; Conservative   46; Mismatches   98; Indels   23; Gaps   9;

Qy   38 YQVGPLLGSGGFGSVYSGIRVSDNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVS 97
              :|:| ||||| |||| ||||:: ||: ::|: :|| :::|:|
Db   1 YELGEKLGSGAFGKVYKGKHKDTGEIVAIKILKCRSLSE-----KKKRFLREIQILRRLS 55

Qy   98 SGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERG-ALQEELARSFFWQVLEAVR 156
              |||| :| |||::|::::|:| |::|::|:| |:| :: | |:|
Db   56 --HPNIVRLLGVFEBDDHJYLVMEYMEG-GDLFDYLRRNGLLLSEKEAKKIALQILRGLE 112

Qy   157 HCHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVY---TDFDGTRVYSPPEWI 213
              :|:||:| :||||:| |||| | ||:|:| :: ||: |: :| |:
Db   113 YLHSRGIVHRDLKPENILLDEN-GTVKIADFGLARKLESSSYEKLTTFVGTPEYMAPEVL 171

Qy   214 RYHRYHGRSAAVWSLGILLYDMVCGDIPF---EHDEEIIRGQVFFRQRV-----SSECQ 264
              : |||:||:||:|| :::||:: :|: ||| ||
Db   172 EGRGYSSK-VDVWSLGVIIYELLTGKLPFPGIDPLEELFRIKERPRLRLPPPNCSEELK 230

Qy   265 HLIRWCLALRPSDRPTFEEIQNHPW 289
              ||:|| |||:|::| |||| ||||
Db   231 DLIKKCLNKDPEKRPTAKEILNHPW 255

RESULT 3
US-10-501-035-357
; Sequence 357, Application US/10501035
; Publication No. US2006004249A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES AND POLYPEPTIDE FOR PREDICTING
; TITLE OF INVENTION: ACTIVITY OF COMPOUNDS THAT INTERACT WITH PROTEIN TYROSINE KINASE
; TITLE OF INVENTION: AND/OR PROTEIN TYROSINE KINASE PATHWAYS
; FILE REFERENCE: D0185 PCT
; CURRENT APPLICATION NUMBER: US/10/501,035
; CURRENT FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: US 60/350,061
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 795
; SOFTWARE: PatentIn version 3.2
;
; SEQ ID NO 357
; LENGTH: 950
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-501-035-357

Query Match   22.5%; Score 376; DB 6; Length 950;
Best Local Similarity   32.4%; Pred. No. 4.3e-26;
Matches   89; Conservative   50; Mismatches 114; Indels   22; Gaps   7;

Qy   38 YQVGPLLGSGGFGSVYSGIRVSDNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVS 97
              :|:| ||||| |||| ||||:: ||: ::|:
Db   44 YDIEGTLGKGNFAVVKLGRHRITKTEVAIKIIDKSQL----DAVNLEKIYREVQIMKMLD 99

Qy   98 SGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRH 157
              |||| :| |||::|::::|:| ||:||
Db   100 --HPHIIKLYQVMETKSMLYLVTEYAKN-GEIFDYLANHGRLNESSEARRKFWQILSAVDY 156

Qy   158 CHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKD-TVYTDFDGTRVYSPPEWIRYH 216
              ||:||:| :||||:| |||| | ||:|:| :|
Db   157 CHGRKIVHRDLKAENLLLD-NNMNIKIADFGFGNFFKSGELLATWCGSPPYAAPEVFEGQ 215

Qy   217 RYHGRSAAVWSLGILLYDMVCGDIPFEHD------EEIIRGQVFFRQRVSSECQHLIRWC 270
              : :|:||:|| :::||:: :|: ||| ||
Db   216 QYEGPQLDIWSMGVVLYVLVCGALPFDGPTLPILRQRVLEGRFRIPYFMSEDCEEHLIRRM 275

Qy   271 LALRPSDRPTFEEIQNHPWM------QDVLLPQE 298
              |||:|::| |||| |||| |:|:|
Db   276 LVLDPSKRLTIAQIKEHKWMLIEVPVQRPVLYPQE 310

RESULT 4
US-11-241-056-11
; Sequence 11, Application US/11241056
; Publication No. US2006024807A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Bird, Timothy A.
; APPLICANT: Virca, G. Duke
; APPLICANT: Martin, Unja
; APPLICANT: Anderson, Dirk M.
; TITLE OF INVENTION: NOVEL MURINE AND HUMAN KINASES
; FILE REFERENCE: 2923-US
; CURRENT APPLICATION NUMBER: US/11/241,056
; CURRENT FILING DATE: 2005-09-30
; PRIOR APPLICATION NUMBER: US/09/980,464
; PRIOR FILING DATE: 2001-11-27
; NUMBER OF SEQ ID NOS: 36

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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 631
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-241-056-11

Query Match         22.1%;    Score 368.5;  DB 7;  Length 631;
Best Local Similarity  33.4%;  Pred. No. 1.2e-25;
Matches    98;  Conservative  46;  Mismatches 116;  Indels  33;  Gaps  9;

Qy   22  ATKLAPGKEKEP------------------LESQYQVGPLLGSGGFGSVYSGIRVSDNLPV  64
             ||  |||                     :|: ||  |||||| | ||  || |
Db   24  ARPLADGLIKSPKPLMKKQAVKRHHHKHNLRHRYEFLETLGKGTYGKVKKA-RESSGRLV  82

Qy   65  AIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFGSVIRLLDWFERPDSFVLILERPE  124
             |||  | |  :|  ||  || || ||||| | |  |||| ||  |  |
Db   83  AIKSIRKDKIKDEQDL--LHIRRELEIMS--SLNHPHIIAIHEVFENSSKIVIVMEYAS  137

Qy  125  PVQDLFDFITERGALQEELARSFFWQVLEAVRHCNCGVLHRDIKDENILIDLNRGELKL  184
             |  |||||||||| |||||||||||||  :|:|||| |||||||| |  |  :|:
Db  138  R-GDLYDYISERPRLSERDARHFFRQIVSALHYCHQNGIVHRDLKLENILLDAN-GNIKI  195

Qy  185  IDFG-SGALLKDTVTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDIPFE  243
             |||   |||| :  |  |  |||  ||||        |||||| :| :| || |:|:
Db  196  ADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVGPEVDSWSLGVLLYILVHGTMPFD  255

Qy  244  HDE------EIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWM  290
                     ||| :  || :|  ||| ||  ||||||  ||  ||| :
Db  256  GQDHKTLVKQISNGAYREPPKPSDAC-GLIRWLLMVNPTRRATLEDVASHWWV  307


RESULT 5
US-11-087-099-9816
; Sequence 9816, Application US/1087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 9816
; LENGTH: 504
; TYPE: PRT
; ORGANISM: Cucumis sativus
US-11-087-099-9816

Query Match         21.9%;    Score 366;  DB 7;  Length 504;
Best Local Similarity  34.4%;  Pred. No. 1.6e-25;
Matches    90;  Conservative  51;  Mismatches 105;  Indels  16;  Gaps  8;

Qy   38  YQVGPLLGSGGFGSVYSGIRVSDNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVS  97
             |||||||||||||||||||||||||:  ||:  :|: : |  :|:
Db    8  YKLGKTLGIGSFGKVKIAEHALTGHKVAIKILNRRKIKN---LDMEEKVRREIKILRLFM  64

Qy   98  SGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRH  157
             |||  |||||| |||||||||||||:  ||||||||||||||||  |:|:|:|
Db   65  --HPHIIRLYEVIETPSDIYVVMEYVKS-GELFDYIVEKGRLQEDEARNFFQQIISGVEY  121

Qy  158  CHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVYTDFD-GTRVYSPPEWIRYH  216
             |||  ||||||||||||||| |  || ||| |  |::  :  |  |||||||||||||
Db  122  CHRNMVVHRDLKPENLLD-SKCNVKIADFGLSNIMRDGHFLKTSCGSPNYAAPEVISGK  180

Qy  217  RYHGRSAAVWSLGILLYDMVCGDIPFEHDEI------IRGQVF-FRQRVSSECQHLIRW  269
             ||||||||||||||||||||:||   |  ||      || |  | ||||||||||||
Db  181  LYAGPEVDVWSCGVILYALLCGTLPFD-DENIPNLFKKIKGGIYTLPSHLSSGARELIPS  239

Qy  270  CLALRPSDRPTFEEIQNHPWMQ  291
             |||||||||| |||  |||| |
Db  240  MLVVDPMKRITIPEIRQHPWFQ  261


RESULT 6
US-10-877-346-72
; Sequence 72, Application US/10877346
; Publication No. US20060014153A1
; GENERAL INFORMATION:
; APPLICANT: Gerlach, Valerie L
; APPLICANT: MacDougall, John R
; APPLICANT: Smithson, Glennda
; APPLICANT: Millet, Isabelle
; APPLICANT: Stone, David
; APPLICANT: Gunther, Erik
; APPLICANT: Ellerman, Karen
; APPLICANT: Grosse, William M
; APPLICANT: Alsobrook II, John P
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine E
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Leach, Martin D
; APPLICANT: Shimkets, Richard A
; TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-124
; CURRENT APPLICATION NUMBER: US/10/877,346
; CURRENT FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US/09/964,956
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/235,631
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/235,633
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/235,808
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,064
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,065
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,066
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,135
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 60/237,434
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/238,321
; PRIOR FILING DATE: 2000-10-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 72
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Serine/Threonine protein kinase Consensus
; OTHER INFORMATION: Sequence
US-10-877-346-72

Query Match         21.8%;    Score 364.5;  DB 6;  Length 256;
Best Local Similarity  33.3%;  Pred. No. 8.9e-26;
Matches    89;  Conservative  55;  Mismatches  96;  Indels  27;  Gaps  8;

Qy   38  YQVGPLLGSGGFGSVYSGIRVSDNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVS  97
             |:: || ||||: : |  |  ||:  :|:|:  :  :|:  :|
Db    1  YELLEVLGKGAFGKVYLARDKKTGKLVAIKVIKKEKL---KKKKRERILREIKILKKLD  56

Qy   98  SGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRH  157
             |||  || :| | ||||  :||:|:||||  |||||||||||||||| :||||||||
Db   57  --HPNIVKLYDVFEDDDKLYLVMEYCEG-GDLFDLLKKRGRLSEDEARFYARQILSALEY  113

Qy  158  CHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKD--TVYTDFDGTRVYSPPEWIRY  215
             |:|||:|||: : || | || ||  | |  | :  |    ::|  |  |||||||||
Db  158  CHNCGVLHRDLIDLNRGELKLIDFGSGALLKD--TVYTDFDGTRVYSPPEWIRY  215
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Db   114 LHSQGIIHRDLKPENILLD-SDGHVKLADFGLAKQLDSGGTLLTTFVGTPEYMAPE-VLL 171

Qy   216 HRYHGRSAAVWSLGILLYDMVCGDIPFEHDEEIIRGQVFFRQ---------RVSSE 262
             : :|:: ||:|::|||| |::| || :|::|
Db   172 GKGYGKAVDIWSLGVILYELLTGKPPFPGDDQLL---ALFKKIGKPPPPPPEWKISPE 228

Qy   263 CQHLIRWCLALRPSDRPTFEEIQNHPW 289
             : ||:| : ||:
Db   229 AKDLIKKLLVKDPEKRLTAEEALEHPF 255

RESULT 7
US-11-113-424-183
; Sequence 183, Application US/11113424
; Publication No. US20050260713A1
; GENERAL INFORMATION:
;   APPLICANT: Gangolli et al.
;   TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
;   FILE REFERENCE: 21402-225
;   CURRENT APPLICATION NUMBER: US/11/113,424
;   CURRENT FILING DATE: 2005-04-21
;   PRIOR APPLICATION NUMBER: 60/256,704
;   PRIOR FILING DATE: 2000-12-19
;   PRIOR APPLICATION NUMBER: 60/311,590
;   PRIOR FILING DATE: 2001-08-10
;   PRIOR APPLICATION NUMBER: 60/257,314
;   PRIOR FILING DATE: 2000-12-20
;   PRIOR APPLICATION NUMBER: 60/311,613
;   PRIOR FILING DATE: 2001-08-10
;   PRIOR APPLICATION NUMBER: 60/315,617
;   PRIOR FILING DATE: 2001-08-29
;   PRIOR APPLICATION NUMBER: 60/307,506
;   PRIOR FILING DATE: 2001-07-24
;   PRIOR APPLICATION NUMBER: 60/322,358
;   PRIOR FILING DATE: 2001-05-29
;   PRIOR APPLICATION NUMBER: 60/294,075
;   PRIOR FILING DATE: 2001-09-14
;   PRIOR APPLICATION NUMBER: 60/288,153
;   PRIOR FILING DATE: 2001-05-02
;   NUMBER OF SEQ ID NOS: 190
;   SEQ ID NO 183
;   LENGTH: 256
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: consensus
;   OTHER INFORMATION: sequence
US-11-113-424-183

Query Match   21.8%; Score 364.5; DB 7; Length 256;
Best Local Similarity   33.3%; Pred. No. 8.9e-26;
Matches   89; Conservative 55; Mismatches 96; Indels 27; Gaps 8;

Qy   38 YQVGPLLGSCGFGSVYSGIRVSDNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVS 97
             |:: |||| ||||:|||| :|: ::||:|||||
Db   1 YELLEVLGKGAFGKVYLARDKKTGKLVAIKVIKKEKL----KKKKRERILREIKILKKLD 56

Qy   98 SGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRH 157
             :::||| | |||:|||:| ::|| | |::::||:||:::: :|
Db   57 --HPNIVKLYDVFEDDDKLYLVMEYCEG-GDLFDLLKKRGRLSEDEARFYARQIISALEY 113

Qy   158 CHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKD--TVYTDFDGTRVYSPPEWIRY 215
             : :|||||||||||||| | |||| ||||:| || ::||:|:: :||||||||
Db   114 LHSQGIIHRDLKPENILLD-SDGHVKLADFGLAKQLDSGGTLLTTFVGTPEYMAPE-VLL 171

Qy   216 HRYHGRSAAVWSLGILLYDMVCGDIPFEHDEEIIRGQVFFRQ---------RVSSE 262
             : :|:: ||:|::|||| |::| || :|::|
Db   172 GKGYGKAVDIWSLGVILYELLTGKPPFPGDDQLL---ALFKKIGKPPPPPPEWKISPE 228

Qy   263 CQHLIRWCLALRPSDRPTFEEIQNHPW 289
             : ||:| : ||:
Db   229 AKDLIKKLLVKDPEKRLTAEEALEHPF 255

RESULT 8
US-11-087-099-11500
; Sequence 11500, Application US/11087099
; Publication No. US2006041961A1
; GENERAL INFORMATION:
;   APPLICANT: Abad, Mark S. et al.
;   TITLE OF INVENTION: Genes and Uses for Plant Improvement
;   FILE REFERENCE: 38-21(53450)B EP
;   CURRENT APPLICATION NUMBER: US/11/087,099
;   CURRENT FILING DATE: 2005-03-22
;   NUMBER OF SEQ ID NOS: 12464
;   SEQ ID NO 11500
;   LENGTH: 514
;   TYPE: PRT
;   ORGANISM: Lycopersicon esculentum
US-11-087-099-11500

Query Match   21.3%; Score 356; DB 7; Length 514;
Best Local Similarity   33.2%; Pred. No. 1.3e-24;
Matches   87; Conservative 54; Mismatches 105; Indels 16; Gaps 8;

Qy   38 YQVGPLLGSCGFGSVYSGIRVSDNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVS 97
             |:: |||| ||||:|||| :|: ::||:|||||
Db   19 YKLGKTLGISFGKVKIAEHTLTGHKVAVKILNRRKIRN---MDMEEKVRREIKILRLFM 75

Qy   98 SGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRH 157
             :::||| | |||:|||:| ::|| | |::::||:||:::: :|
Db   76 --HPHIIRLYEVIETPSDIYVMEYVKS-GELFDYIVEKGRLQEDEARNFFQQIISGVEY 132

Qy   158 CHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVYTDFD-GTRVYSPPEWIRYH 216
             : :|||||||||| ::|: :|: :||||:| :::|| ::|:::||:
Db   133 CHRNMVVHRDLKPENLLLD-SKWNVKIADFGLSNIMRDGHFLKTSCGSPNYAAPEVISGK 191

Qy   217 RYHGRSAAVWSLGILLYDMVCGDIPFEHDEEI------IRGQVF-FRQRVSSECQHLIRW 269
             ||:|:: ||:|::|||| |::| :::|| |::
Db   192 LYAGPEVDVWSCGVILYALLCGTLPFD-DENIPNLFKKIKGGIYTLPSHLSAGARDLIPR 250

Qy   270 CLALRPSDRPTFEEIQNHPWMQ 291
             ||| | ||:
Db   251 MLIVDPMKRWTIPEIRLHPWFQ 272

RESULT 9
US-11-087-099-3997
; Sequence 3997, Application US/11087099
; Publication No. US2006041961A1
; GENERAL INFORMATION:
;   APPLICANT: Abad, Mark S. et al.
;   TITLE OF INVENTION: Genes and Uses for Plant Improvement
;   FILE REFERENCE: 38-21(53450)B EP
;   CURRENT APPLICATION NUMBER: US/11/087,099
;   CURRENT FILING DATE: 2005-03-22
;   NUMBER OF SEQ ID NOS: 12464
;   SEQ ID NO 3997
;   LENGTH: 512
;   TYPE: PRT
;   ORGANISM: Solanum tuberosum
US-11-087-099-3997

Query Match   21.1%; Score 352; DB 7; Length 512;
Best Local Similarity   32.2%; Pred. No. 3.1e-24;
Matches   84; Conservative 55; Mismatches 108; Indels 14; Gaps 6;

Qy   38 YQVGPLLGSCGFGSVYSGIRVSDNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVS 97
             |:: |||| ||||:|||| :|: ::||:|||||
Db   19 YKLGKTLGISFGKVKIAEHTLIGHKVAVKILNRRKIRN---MDMEEKVSREIKILRLFM 75

Qy   98 SGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRH 157
             :::||| | |||:|||:| ::|| | |::::||:||:::: :|
Db   76 HGH--ISRLYEVIETPSDIYVMEYVKS-GELFDYIVEKGRLQEDEARNFFQQIISGVEY 132

```
Qy  158 CHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVYTDFD-GTRVYSPPEWIRYH 216
Db  133 CHINMVHRDLKPENLLLD-SKWNVKIADFGLSNIMRDGHFLKTSCGSPNYAAPEVISGK  191
Qy  217 RYHGRSAAVWSLGILLYDMVCGDIPFEHD-----EEIIRGQVFFRQRVSSECQHLIRWC  270
Db  192 LYAGPEVDVWSCGVILYALLCGTLPFDDENIPNLFKKIKGGYITLPSHLSAGARDLIPRM 251
Qy  271 LALRPSDRPTFEEIQNHPWMQ 291
Db  252 LIVDPMKRMTIPEIRLHPWFQ 272
```

RESULT 10
US-11-087-099-3612
; Sequence 3612, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 3612
; LENGTH: 514
; TYPE: PRT
; ORGANISM: Solanum tuberosum
US-11-087-099-3612

Query Match   21.1%; Score 352; DB 7; Length 514;
Best Local Similarity   32.2%; Pred. No. 3.1e-24;
Matches   84; Conservative 55; Mismatches 108; Indels 14; Gaps   6;

```
Qy   38 QYQVGPLLGSGGFGSVYSGIRVSDNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVS 97
Db   19 YKLGKTLGIGSFGKVKIAEHTLIGHKVAVKILNRRKIRN---MDMEEKVSREIKILRLFM  75
Qy   98 SGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRH 157
Db   76 HGH--ISRLYEVIETPSDIYVMEYKS-GELFDYIVEKGRLQEDEARNFFQQIISGVEY   132
Qy  158 CHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVYTDFD-GTRVYSPPEWIRYH 216
Db  133 CHINMVHRDLKPENLLLD-SKWNVKIADFGLSNIMRDGHFLKTSCGSPNYAAPEVISGK  191
Qy  217 RYHGRSAAVWSLGILLYDMVCGDIPFEHD-----EEIIRGQVFFRQRVSSECQHLIRWC  270
Db  192 LYAGPEVDVWSCGVILYALLCGTLPFDDENIPNLFKKIKGGYITLPSHLSAGARDLIPRM 251
Qy  271 LALRPSDRPTFEEIQNHPWMQ 291
Db  252 LIVDPMKRMTIPEIRLHPWFQ 272
```

RESULT 11
US-11-087-099-12402
; Sequence 12402, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 12402
; LENGTH: 619
; TYPE: PRT
; ORGANISM: Candida tropicalis
US-11-087-099-12402

Query Match   20.9%; Score 348.5; DB 7; Length 619;
Best Local Similarity   31.0%; Pred. No. 8.2e-24;
Matches   86; Conservative 57; Mismatches 115; Indels 19; Gaps   7;

```
Qy   37 QYQVGPLLGSGGFGSVYSGIRVSDNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKV  96
Db   51 RYQIIKTLGEGSFGKVKLAQHVGTGQKVALKIINRKTLA---KSDMQGRVEREISYLRLL 107
Qy   97 SSGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELARSFFWQVLEAVR 156
Db  108 R--HPHIIKLYDVIKSDEIIMVIEFAG--KELFDYIVQRGKMPEDEARRFFQQIIAAVE  163
Qy  157 HCHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVYTDFD-GTRVYSPPEWIRY 215
Db  164 YCHRHKIVHRDLKPENLLLD-DQLNVKIADFGLSNIMTDGNFLKTSCGSPNYAAPEVISG 222
Qy  216 HRYHGRSAAVWSLGILLYDMVCGDIPFEHD-----EEIIRGQVFFRQRVSSECQHLIRW  269
Db  223 KLYAGPEVDVWSSGVILYVMLCCRLPFDDEFIPALFKKISNGVYTLPNVLSPGAKHLLTR 282
Qy  270 CLALRPSDRPTFEEIQNHPW---MQDVLLPQETAEI 302
Db  283 MLVVNPLNRITIHEIMEDEWFKQDMPDYLLPPDLSKI 319
```

RESULT 12
US-11-087-099-11838
; Sequence 11838, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 11838
; LENGTH: 472
; TYPE: PRT
; ORGANISM: Guillardia theta
US-11-087-099-11838

Query Match   20.8%; Score 348; DB 7; Length 472;
Best Local Similarity   32.3%; Pred. No. 6.4e-24;
Matches   92; Conservative 49; Mismatches 118; Indels 26; Gaps   9;

```
Qy   18 NDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSDNLPVAIKHVEKDRISDW  77
Db    2 NKLFSIKIGP----------YYLGKTLGVGSFGKVKLGEHELCGQKVAVKILNRKKIKN-  50
Qy   78 GELPNGTRVPMEVVLLKKVSSSGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERG 137
Db   51 --LKMEEKVKREICILKLFM--HPHIIRLYEVIETPTDIFVVTEYITG-GELFDYIVERG 105
Qy  138 ALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTV 197
Db  106 RLNEDESRKFPQQMISGIEYCHNHMVVHRDLKPENILLDAHL-NVKIADFGLSNIMKDGN 164
Qy  198 YTDFD-GTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDIPFEHDEEI------IR 250
Db  165 FLKTSCGSPNYAAPEVINGKSYLGPEVDVWSCGVIMYALLCGSLPFD-DENIPNLFKKIK 223
Qy  251 GQVFFRQRVSSE-CQHLIRWCLALRPSDRPTFEEIQNHPWMQDVL 294
Db  224 SGIYILPGYLSDLSRDMIAKMLITNPLLRITINEIRDHPWFNSRL 268
```

RESULT 13
US-10-770-726-67
; Sequence 67, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene

```
;  APPLICANT: Liu, Wei
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
   CANCERS
;  FILE REFERENCE: AM101079 (031896-010000)
;  CURRENT APPLICATION NUMBER: US/10/770,726
;  CURRENT FILING DATE: 2004-02-04
;  NUMBER OF SEQ ID NOS: 48640
;  SOFTWARE: PatentIn version 3.2
;  SEQ ID NO 67
;  LENGTH: 651
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-10-770-726-67

Query Match             20.5%;   Score 342.5; DB 6;   Length 651;
Best Local Similarity   33.2%;   Pred. No. 3.1e-23;
Matches   97; Conservative   51; Mismatches  117; Indels   27; Gaps   10;

Qy    29 KEKEPLESQYQVGPLLGSGGFGSVYSGIRVSDNLPVAIKHVEKDRISDWGELPNGTRVPM 88
         |::: ::|||:|  :|:|||||::: ||:||
Db     2 KDYDELLKYELHETIGTGFAKVKLACHILTGEMVAIKIMDKNTLG---SDLP---RIKT 56

Qy    89 EVVLLKKVSSGFSGVIRLLDWFERPDSFVLILERPEPVQDLPFITERGALQEELARSFF 148
         :|||  ::||| |:||||||
Db    57 EIEEALKNLR--HQHICQLYHVLETANKIFMVLEYC-PGGGLFDYIISQDRLSEEETRVVF 113
```

```
RESULT 14
US-11-177-138-10
;  Sequence 10, Application US/11177138
;  Publication No. US2005028766A1
;  GENERAL INFORMATION:
;  APPLICANT: Wu, Bin
;  APPLICANT: Seeley, Todd
;  APPLICANT: Williams, Lewis T.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING NEOPLASTIC DISEASE USING
   CHEMOTHERAPY AND RADIATION SENSITIZERS
;  FILE REFERENCE: 200130.514/PP-01623.002
;  CURRENT APPLICATION NUMBER: US/11/177,138
;  CURRENT FILING DATE: 2005-07-08
;  PRIOR APPLICATION NUMBER: US/09/870,937
;  PRIOR FILING DATE: 2001-05-30
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: FastSEQ for Windows Version 3.0
;  SEQ ID NO 10
;  LENGTH: 651
;  TYPE: PRT
;  ORGANISM: Homo sapien
US-11-177-138-10

Query Match             20.5%;   Score 342.5; DB 7;   Length 651;
Best Local Similarity   33.2%;   Pred. No. 3.1e-23;
Matches   97; Conservative   51; Mismatches  117; Indels   27; Gaps   10;

Qy    29 KEKEPLESQYQVGPLLGSGGFGSVYSGIRVSDNLPVAIKHVEKDRISDWGELPNGTRVPM 88
         |::: ::|||:|  :|:|||||::: ||:||
Db     2 KDYDELLKYELHETIGTGFAKVKLACHILTGEMVAIKIMDKNTLG---SDLP---RIKT 56

Qy    89 EVVLLKKVSSGFSGVIRLLDWFERPDSFVLILERPEPVQDLPFITERGALQEELARSFF 148
         :|||  ::||| |:||||||
Db    57 EIEEALKNLR--HQHICQLYHVLETANKIFMVLEYC-PGGGLFDYIISQDRLSEEETRVVF 113
```

```
Qy   149 WQVLEAVRHCHCNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVTDFD-----G 203
         :  | | |::|||||| |:|| | ||
Db   114 RQIVSAVAYVHSQGYAHRDLKPENLLFD-EYHKLKLIDFGLCAKPKGN--KDYHLQTCCG 170

Qy   204 TRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDIPFEHD------EEIIRGQVFFRQ 257
         :|:: :||||||||| :|||||
Db   171 SLAYAAPELIQGKSYLGSEADVWSMGILLYVLMCGFLPFDDDNVMALYKKIMRGKYDVPK 230

Qy   258 RVSSECQHLIRWCLALRPSDRPTFEEIQNHPW-MQDVLLPQETAE----IHL 304
         ||:: |::|||| | ||||
Db   231 WLSPSSILLQQMLQVDPKKRISMKNLLNHPWIMQDYNYPVEWQSKNPFIHL 282
```

```
RESULT 15
US-11-096-568A-22124
;  Sequence 22124, Application US/11096568A
;  Publication No. US20060048240A1
;  GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION: Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE: 2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
;  SEQ ID NO 22124
;  LENGTH: 464
;  TYPE: PRT
;  ORGANISM: Zea mays subsp. mays
;  FEATURE:
;  NAME/KEY: misc_feature
;  LOCATION: (1)..(464)
;  OTHER INFORMATION: Ceres Seq. ID no. 12407640
US-11-096-568A-22124

Query Match             20.5%;   Score 342; DB 7;   Length 464;
Best Local Similarity   30.9%;   Pred. No. 2.2e-23;
Matches   93; Conservative   48; Mismatches  112; Indels   48; Gaps    7;

Qy    28 GKEKEPLESQ------------YQVGPLLGSGGFGSVY-----SGIRVSDNLPVAIKHVEKDRI 74
         |:||| ||:|                ||:| ||::          ||:||:      ::|::
Db     5 GREAEPGEEERKLVLGKYELGRLLGGTFAKVYYARDLSAGAGTGHSCSVAIKVIDKARL 64

Qy    75 SDWGELPNGTRVPM-----EVVLLKKVSSGFSGVIRLLDWFERPDSFVLILERPEP 125
         :|||:||||:||
Db    65 RRTEGMVEQLRREISIMRMVRHPNVVGIREVLASRSRVFVVMEYARGGELFAKV------ 118

Qy   126 VQDLPFITERGALQEELARSFFWQVLEAVRHCNCGVLHRDIKDENILIDLNRGELKLI 185
                         ||:|||:|  :|:::  :::||||| |:|| |||:|
Db   119 ------ARGRLDEDHARRYFQQLVAAVGFCHRRGVAHRDLKPENLLLD--EAGRLKVT 168

Qy   186 DFGSGALLK---DTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDIP 241
         ||| ||||       :: |:|:|: :||||:: :||:|||||:||||
Db   169 DFGLAALPEQLRHDGLLHTCGTPAYVAPEVLRKRGYDGARADLWSCGVVLYVLLCGFLP 228

Qy   242 FEHDEIIRGQVFFRQR--------VSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLL 295
         |:||  ::  ::  :           ||   :||  :: :: ||    ||:: |:||
Db   229 FQHDNYVKLYQKIFKADYQVPPWVSGDARRLIARLLVVDPAKRASIAEIMCTPWFRKGFV 288

Qy   296 P 296
         |
Db   289 P 289
```

Search completed: April 21, 2006, 13:14:14
Job time : 27 secs

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                    GenCore version 5.1.7
            Copyright (c) 1993 - 2006  Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on:      April 21, 2006, 13:10:04 ; Search time 166 Seconds
                                (without alignments)
                             787.835 Million cell updates/sec

Title:      US-10-664-421-1
Perfect score:  1670
Sequence:   1 MLLSKINSLAHLRAAPCNDL.........LLPQETABIHLSLSPGPSK 313

Scoring table:  BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched:    1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters:    1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :     Published Applications AA Main:*
          1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
          2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
          3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
          4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
          5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
          6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	1670	100.0	313	3	US-09-971-791-9	Sequence 9, Appli
2	1670	100.0	313	4	US-10-081-119-18	Sequence 18, Appli
3	1670	100.0	313	4	US-10-394-322A-52	Sequence 52, Appli
4	1670	100.0	313	4	US-10-348-081-13	Sequence 13, Appli
5	1670	100.0	313	4	US-10-664-421-1	Sequence 1, Appli
6	1670	100.0	313	4	US-10-664-421-150	Sequence 150, App
7	1670	100.0	313	4	US-10-705-757-2	Sequence 2, Appli
8	1670	100.0	313	4	US-10-377-268-9	Sequence 9, Appli
9	1670	100.0	313	5	US-10-951-389-18	Sequence 18, Appli
10	1670	100.0	313	5	US-10-951-406-18	Sequence 18, Appli
11	1670	100.0	313	5	US-10-951-477-18	Sequence 18, Appli
12	1670	100.0	313	5	US-10-977-087-18	Sequence 18, Appli
13	1670	100.0	313	5	US-10-941-635-1	Sequence 1, Appli
14	1670	100.0	313	4	US-10-941-635-152	Sequence 152, App
15	1657	99.2	313	4	US-10-620-052A-22	Sequence 22, Appl
16	1636	98.0	313	3	US-09-971-791-8	Sequence 8, Appli
17	1636	98.0	313	4	US-10-348-081-12	Sequence 12, Appli
18	1636	98.0	313	4	US-10-705-757-4	Sequence 4, Appli
19	1582	94.7	313	3	US-09-971-791-7	Sequence 7, Appli
20	1582	94.7	313	4	US-10-348-081-14	Sequence 14, Appli
21	1582	94.7	313	4	US-10-664-421-2	Sequence 2, Appli
22	1582	94.7	313	4	US-10-705-757-6	Sequence 6, Appli
23	1582	94.7	313	4	US-10-377-268-10	Sequence 10, Appli
24	1582	94.7	313	5	US-10-941-635-2	Sequence 2, Appli
25	1362	81.6	253	4	US-10-620-052A-71	Sequence 71, Appli
26	1140	68.3	323	3	US-10-664-421-7	Sequence 7, Appli
27	1140	68.3	323	4	US-10-377-268-15	Sequence 15, Appli
28	1140	68.3	323	5	US-10-941-635-7	Sequence 7, Appli
29	1135	68.0	374	4	US-10-425-114-54275	Sequence 54275, A
30	1133	67.8	326	3	US-09-971-791-2	Sequence 2, Appli
31	1133	67.8	326	4	US-10-348-081-2	Sequence 2, Appli
32	1133	67.8	326	4	US-10-664-421-166	Sequence 166, App
33	1133	67.8	374	4	US-10-618-941-82	Sequence 82, Appl
34	1133	67.8	374	4	US-10-425-114-54264	Sequence 54264, A
35	1129.5	67.6	326	4	US-10-348-081-6	Sequence 6, Appli
36	1129.5	67.6	326	4	US-10-705-757-11	Sequence 11, Appl
37	1129.5	67.6	326	4	US-10-377-268-14	Sequence 14, Appl
38	1129.5	67.6	326	5	US-10-941-635-6	Sequence 6, Appli
39	1128.5	67.6	326	4	US-10-348-081-10	Sequence 10, Appl
40	1128.5	67.6	326	4	US-10-705-757-9	Sequence 9, Appli
41	1128.5	67.6	455	3	US-09-971-791-5	Sequence 5, Appli
42	1116	66.8	325	4	US-10-664-421-6	Sequence 6, Appli
43	1105	66.2	323	3	US-09-971-791-6	Sequence 6, Appli
44	1105	66.2	323	4	US-10-348-081-11	Sequence 11, Appl
45	1105	66.2	323	4	US-10-664-421-8	Sequence 8, Appli

ALIGNMENTS

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RESULT 1
US-09-971-791-9
; Sequence 9, Application US/09971791
; Patent No. US2002011512OA1
; GENERAL INFORMATION:
;   APPLICANT: Rosanna Kapeller-Libermann
;   APPLICANT: Laura A. Rudolph-Owen
;   APPLICANT: Kyle MacBeth
;   TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY AND USES TH
;   FILE REFERENCE: 35800/238856
;   CURRENT APPLICATION NUMBER: US/09/971,791
;   CURRENT FILING DATE: 2001-10-04
;   PRIOR APPLICATION NUMBER: 09/644,450
;   PRIOR FILING DATE: 2000-08-23
;   PRIOR APPLICATION NUMBER: 09/237,543
;   PRIOR FILING DATE: 1999-01-26
;   NUMBER OF SEQ ID NOS: 11
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
;   LENGTH: 313
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-971-791-9

  Query Match             100.0%;  Score 1670;  DB 3;  Length 313;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-143;
  Matches  313;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy     61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy    121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy    181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy    241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy    301 EIHLHSLSPGPSK 313
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Db      301 EIHLHSLSPGPSK 313

RESULT 2
US-10-081-119-18
; Sequence 18, Application US/10081119
; Publication No. US20030045491A1
; GENERAL INFORMATION:
;  APPLICANT: Reinhard, Christoph
;  APPLICANT: Jefferson, Anne B.
;  APPLICANT: Chan, Vivien W.
;  TITLE OF INVENTION: TTK in Diagnosis and as a Therapeutic
;  TITLE OF INVENTION: Target in Cancer
;  FILE REFERENCE: 16932.002
;  CURRENT APPLICATION NUMBER: US/10/081,119
;  CURRENT FILING DATE:  2002-02-21
;  PRIOR APPLICATION NUMBER: 60/289,813
;  PRIOR FILING DATE: 2001-02-21
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-081-119-18

Query Match             100.0%;  Score 1670;  DB 4;  Length 313;
Best Local Similarity   100.0%;  Pred. No. 2.2e-143;
Matches   313;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy       61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy      121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy      181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy      241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy      301 EIHLHSLSPGPSK 313
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Db      301 EIHLHSLSPGPSK 313

RESULT 3
US-10-394-322A-52
; Sequence 52, Application US/10394322A
; Publication No. US20030232391A1
; GENERAL INFORMATION:
;  APPLICANT: SUNESIS PHARMACEUTICALS, INC.
;  APPLICANT: Prescott, John C.
;  TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS
;  FILE REFERENCE: 39750-0006 US
;  CURRENT APPLICATION NUMBER: US/10/394,322A
;  CURRENT FILING DATE:  2003-03-20
;  PRIOR APPLICATION NUMBER: US 60/366,892
;  PRIOR FILING DATE: 2002-03-21
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-394-322A-52

Query Match             100.0%;  Score 1670;  DB 4;  Length 313;
Best Local Similarity   100.0%;  Pred. No. 2.2e-143;
Matches   313;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
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Db        1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy       61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy      121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy      181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy      241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy      301 EIHLHSLSPGPSK 313
            |||||||||||||
Db      301 EIHLHSLSPGPSK 313

RESULT 4
US-10-348-081-13
; Sequence 13, Application US/10348081
; Publication No. US20040038246A1
; GENERAL INFORMATION:
;  APPLICANT: KORN, Marcus
;  APPLICANT: MUELLER, Guenter
;  APPLICANT: SCHNEIDER, Rudolf
;  APPLICANT: TSCHANK, Georg
;  TITLE OF INVENTION: PIM-3 KINASE AS A TARGET FOR TYPE 2 DIABETES MELLITUS
;  FILE REFERENCE: DEAV2002/0004 US NP
;  CURRENT APPLICATION NUMBER: US/10/348,081
;  CURRENT FILING DATE:  2003-01-21
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-348-081-13

Query Match             100.0%;  Score 1670;  DB 4;  Length 313;
Best Local Similarity   100.0%;  Pred. No. 2.2e-143;
Matches   313;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy       61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy      121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy      181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
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; ORGANISM: Homo sapiens
US-10-394-322A-52

Qy   241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy   301 EIHLHSLSPGPSK 313
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Db   301 EIHLHSLSPGPSK 313

RESULT 5
US-10-664-421-1
; Sequence 1, Application US/10664421
; Publication No. US2004142864A1
; GENERAL INFORMATION:
;   APPLICANT: BREMER, RYAN
;   APPLICANT: IBRAHIM, PRABHA
;   APPLICANT: KUMAR, ABHINAV
;   APPLICANT: MANDIYAN, VALSAN
;   APPLICANT: MILBURN, MICHAEL V.
;   TITLE OF INVENTION: CRYSTAL STRUCTURE OF PIM-1 KINASE
;   FILE REFERENCE: 039363/0703
;   CURRENT APPLICATION NUMBER: US/10/664,421
;   CURRENT FILING DATE: 2003-09-16
;   PRIOR APPLICATION NUMBER: 60/412,341
;   PRIOR FILING DATE: 2002-09-20
;   PRIOR APPLICATION NUMBER: 60/411,398
;   PRIOR FILING DATE: 2002-09-16
;   NUMBER OF SEQ ID NOS: 169
;   SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 1
;   LENGTH: 313
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-664-421-1

Query Match   100.0%; Score 1670; DB 4; Length 313;
Best Local Similarity   100.0%; Pred. No. 2.2e-143;
Matches   313; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD   60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD   60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy   241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy   301 EIHLHSLSPGPSK 313
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Db   301 EIHLHSLSPGPSK 313

RESULT 6
US-10-664-421-150
; Sequence 150, Application US/10664421
; Publication No. US2004142864A1
; GENERAL INFORMATION:
;   APPLICANT: BREMER, RYAN
;   APPLICANT: IBRAHIM, PRABHA
;   APPLICANT: KUMAR, ABHINAV
;   APPLICANT: MANDIYAN, VALSAN
;   APPLICANT: MILBURN, MICHAEL V.
;   TITLE OF INVENTION: CRYSTAL STRUCTURE OF PIM-1 KINASE
;   FILE REFERENCE: 039363/0703
;   CURRENT APPLICATION NUMBER: US/10/664,421
;   CURRENT FILING DATE: 2003-09-16
;   PRIOR APPLICATION NUMBER: 60/412,341
;   PRIOR FILING DATE: 2002-09-20
;   PRIOR APPLICATION NUMBER: 60/411,398
;   PRIOR FILING DATE: 2002-09-16
;   NUMBER OF SEQ ID NOS: 169
;   SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 150
;   LENGTH: 313
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-664-421-150

Query Match   100.0%; Score 1670; DB 4; Length 313;
Best Local Similarity   100.0%; Pred. No. 2.2e-143;
Matches   313; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD   60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD   60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy   241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy   301 EIHLHSLSPGPSK 313
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Db   301 EIHLHSLSPGPSK 313

RESULT 7
US-10-705-757-2
; Sequence 2, Application US/10705757
; Publication No. US20040146942A1
; GENERAL INFORMATION:
;   APPLICANT: GRUENENTHAL GMBH
;   TITLE OF INVENTION: SCREENING METHOD USING PIM1-KINASE OR PIM3-KINASE
;   FILE REFERENCE: 029310.52818US
;   CURRENT APPLICATION NUMBER: US/10/705,757
;   CURRENT FILING DATE: 2003-11-12
;   PRIOR APPLICATION NUMBER: PCT/EP02/05234
;   PRIOR FILING DATE: 2002-05-13
;   PRIOR APPLICATION NUMBER: DE 101 23 055.9
;   PRIOR FILING DATE: 2001-05-11
;   NUMBER OF SEQ ID NOS: 11
;   SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 313
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-705-757-2

Query Match   100.0%; Score 1670; DB 4; Length 313;
Best Local Similarity   100.0%; Pred. No. 2.2e-143;
Matches   313; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD   60

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Db       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSSGGFGSVYSGIRVSD 60
Qy    61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
Qy   121 ERREPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ERREPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
Qy   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
Qy   241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
Qy   301 EIHLHSLSPGPSK 313
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Db   301 EIHLHSLSPGPSK 313
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RESULT 8
US-10-377-268-9
; Sequence 9, Application US/10377268
; Publication No. US2004171062A1
; GENERAL INFORMATION:
; APPLICANT: HIRTH, KLAUS-PETER
; APPLICANT: MILBURN, MICHAEL VANCE
; TITLE OF INVENTION: METHOD FOR THE DESIGN OF MOLECULAR SCAFFOLDS AND LIGANDS
; FILE REFERENCE: 039363/0303
; CURRENT APPLICATION NUMBER: US/10/377,268
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: 60/437,929
; PRIOR FILING DATE: 2003-01-02
; PRIOR APPLICATION NUMBER: 60/360,651
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/411,398
; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 60/412,341
; PRIOR FILING DATE: 2002-09-20
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-377-268-9

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Query Match       100.0%;   Score 1670;  DB 4;   Length 313;
Best Local Similarity  100.0%;   Pred. No. 2.2e-143;
Matches 313;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy     1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSSGGFGSVYSGIRVSD 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSSGGFGSVYSGIRVSD 60
Qy    61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
Qy   121 ERREPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ERREPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
Qy   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
Qy   241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
Qy   301 EIHLHSLSPGPSK 313
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Db   301 EIHLHSLSPGPSK 313
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RESULT 9
US-10-951-389-18
; Sequence 18, Application US/10951389
; Publication No. US2005058627A1
; GENERAL INFORMATION:
; APPLICANT: Reinhard, Christoph
; APPLICANT: Jefferson, Anne B.
; APPLICANT: Chan, Vivien W.
; TITLE OF INVENTION: TTK in Diagnosis and as a Therapeutic
; TITLE OF INVENTION: Target in Cancer
; FILE REFERENCE: 16932.002
; CURRENT APPLICATION NUMBER: US/10/951,389
; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: US/10/081,119
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/289,813
; PRIOR FILING DATE: 2001-02-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-951-389-18

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Query Match       100.0%;   Score 1670;  DB 5;   Length 313;
Best Local Similarity  100.0%;   Pred. No. 2.2e-143;
Matches 313;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy     1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSSGGFGSVYSGIRVSD 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSSGGFGSVYSGIRVSD 60
Qy    61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
Qy   121 ERREPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ERREPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
Qy   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
Qy   241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
Qy   301 EIHLHSLSPGPSK 313
         |||||||||||||
Db   301 EIHLHSLSPGPSK 313
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RESULT 10
US-10-951-406-18
; Sequence 18, Application US/10951406
; Publication No. US2005059630A1
; GENERAL INFORMATION:
; APPLICANT: Reinhard, Christoph
; APPLICANT: Jefferson, Anne B.
; APPLICANT: Chan, Vivien W.
; TITLE OF INVENTION: TTK in Diagnosis and as a Therapeutic
; TITLE OF INVENTION: Target in Cancer
; FILE REFERENCE: 16932.002
; CURRENT APPLICATION NUMBER: US/10/951,406

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; CURRENT FILING DATE:       2004-09-27
; PRIOR APPLICATION NUMBER: US/10/081,119
; PRIOR FILING DATE:         2002-02-21
; PRIOR APPLICATION NUMBER:  60/289,813
; PRIOR FILING DATE:         2001-02-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-951-406-18

Query Match           100.0%;    Score 1670;  DB 5;  Length 313;
Best Local Similarity 100.0%;    Pred. No. 2.2e-143;
Matches  313;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy     1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy    61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy   241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy   301 EIHLHSLSPGPSK 313
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Db   301 EIHLHSLSPGPSK 313


RESULT 12
US-10-977-087-18
; Sequence 18, Application US/10977087
; Publication No. US20050130926A1
; GENERAL INFORMATION:
; APPLICANT: Reinhard, Christoph
; APPLICANT: Jefferson, Anne B.
; APPLICANT: Chan, Vivien W.
; APPLICANT: Kaufmann, Joerg
; APPLICANT: Xin, Hong
; APPLICANT: Kennedy, Giulia C.
; APPLICANT: Khoja, Hamiduddin
; APPLICANT: Shyamala, Venkatakrishna
; TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED IN CANCEROUS CELLS
; TITLE OF INVENTION:  AND THEIR METHODS OF USE V
; FILE REFERENCE: 2300-21986
; CURRENT APPLICATION NUMBER: US/10/977,087
; CURRENT FILING DATE:       2004-10-28
; PRIOR APPLICATION NUMBER:  10/081,119
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/271,254
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 10/360,848
; PRIOR FILING DATE: 2003-02-06
; PRIOR APPLICATION NUMBER: 09/570,593
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: 60/134,112
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 10/763,692
; PRIOR FILING DATE: 2004-01-22
; PRIOR APPLICATION NUMBER: 09/626,301
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: 60/148,936
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: 60/145,612
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: 10/698,959
; PRIOR FILING DATE: 2003-10-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-977-087-18

Query Match           100.0%;    Score 1670;  DB 5;  Length 313;
Best Local Similarity 100.0%;    Pred. No. 2.2e-143;
Matches  313;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
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RESULT 11
US-10-951-477-18
; Sequence 18, Application US/10951477
; Publication No. US20050063974A1
; GENERAL INFORMATION:
; APPLICANT: Reinhard, Christoph
; APPLICANT: Jefferson, Anne B.
; APPLICANT: Chan, Vivien W.
; TITLE OF INVENTION: TTK in Diagnosis and as a Therapeutic
; TITLE OF INVENTION:  Target in Cancer
; FILE REFERENCE: 16932.002
; CURRENT APPLICATION NUMBER: US/10/951,477
; CURRENT FILING DATE:       2004-09-27
; PRIOR APPLICATION NUMBER: US/10/081,119
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/289,813
; PRIOR FILING DATE: 2001-02-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-951-477-18

Query Match           100.0%;    Score 1670;  DB 5;  Length 313;
Best Local Similarity 100.0%;    Pred. No. 2.2e-143;
Matches  313;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy     1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy 241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
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RESULT 13
US-10-941-635-1
; Sequence 1, Application US/10941635
; Publication No. US20050164300A1
; GENERAL INFORMATION:
;   APPLICANT: ARTIS, DEAN R.
;   APPLICANT: BREMER, RYAN E.
;   APPLICANT: GILLETTE, SAMUEL J.
;   APPLICANT: HURT, CLARENCE R.
;   APPLICANT: IBRAHIM, PRABHA L.
;   APPLICANT: ZUCKERMAN, REBECCA L.
;   TITLE OF INVENTION: MOLECULAR SCAFFOLDS FOR KINASE LIGAND DEVELOPMENT
;   FILE REFERENCE: 039363-1702
;   CURRENT APPLICATION NUMBER: US/10/941,635
;   CURRENT FILING DATE: 2004-09-15
;   PRIOR APPLICATION NUMBER: 60/503,277
;   PRIOR FILING DATE: 2003-09-15
;   NUMBER OF SEQ ID NOS: 167
;   SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 1
;   LENGTH: 313
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-941-635-1

Query Match   100.0%; Score 1670; DB 5; Length 313;
Best Local Similarity   100.0%; Pred. No. 2.2e-143;
Matches   313; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy  61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy 121 ERPEPVQDLFDFITTERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 ERPEPVQDLFDFITTERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy 181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy 241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy 301 EIHLHSLSPGPSK 313
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Db 301 EIHLHSLSPGPSK 313
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RESULT 14
US-10-941-635-152
; Sequence 152, Application US/10941635
; Publication No.US20050164300A1
; GENERAL INFORMATION:
;   APPLICANT: ARTIS, DEAN R.
;   APPLICANT: BREMER, RYAN E.
;   APPLICANT: GILLETTE, SAMUEL J.
;   APPLICANT: HURT, CLARENCE R.
;   APPLICANT: IBRAHIM, PRABHA L.
;   APPLICANT: ZUCKERMAN, REBECCA L.
;   TITLE OF INVENTION: MOLECULAR SCAFFOLDS FOR KINASE LIGAND DEVELOPMENT
;   FILE REFERENCE: 039363-1702
;   CURRENT APPLICATION NUMBER: US/10/941,635
;   CURRENT FILING DATE: 2004-09-15
;   PRIOR APPLICATION NUMBER: 60/503,277
;   PRIOR FILING DATE: 2003-09-15
;   NUMBER OF SEQ ID NOS: 167
;   SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 152
;   LENGTH: 313
;   TYPE: PRT
;   ORGANISM: Unknown Organism
;   FEATURE:
;   OTHER INFORMATION: Description of Unknown Organism: Mammalian
;   OTHER INFORMATION: protein sequence
US-10-941-635-152

Query Match   100.0%; Score 1670; DB 5; Length 313;
Best Local Similarity   100.0%; Pred. No. 2.2e-143;
Matches   313; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy  61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy 121 ERPEPVQDLFDFITTERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 ERPEPVQDLFDFITTERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy 181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy 241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy 301 EIHLHSLSPGPSK 313
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Db 301 EIHLHSLSPGPSK 313
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RESULT 15
US-10-620-052A-22
; Sequence 22, Application US/10620052A
; Publication No US20040126784A1
; GENERAL INFORMATION:
;   APPLICANT: Hitoshi, Yasunichi
;   APPLICANT: Jenkins, Yonchu
;   APPLICANT: Markovtsov, Vadim
;   APPLICANT: Rigel Pharmaceuticals, Inc.

```
;   TITLE OF INVENTION: Modulators of Cellular Proliferation
;   FILE REFERENCE: 021044-0040100S
;   CURRENT APPLICATION NUMBER: US/10/620,052A
;   CURRENT FILING DATE: 2003-07-14
;   PRIOR APPLICATION NUMBER: US 60/395,443
;   PRIOR FILING DATE: 2002-07-12
;   NUMBER OF SEQ ID NOS: 78
;   SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
;   LENGTH: 313
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: PIM1 oncogene serine threonine kinase
US-10-620-052A-22

Query Match        99.2%;    Score 1657;   DB 4;    Length 313;
Best Local Similarity  99.4%;  Pred. No. 3.3e-142;
Matches   311;  Conservative   0;  Mismatches   2;  Indels   0;  Gaps   0;

Qy    1  MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD  60
            |||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db    1  MLLSKINSLAHLRARACNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD  60

Qy   61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL  120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL  120

Qy  121  ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG  180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG  180

Qy  181  ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI  240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI  240

Qy  241  PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA  300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241  PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA  300

Qy  301  EIHLHSLSPGPSK  313
            |||||||||||||
Db  301  EIHLHSLSPGPSK  313


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Job time : 167 secs
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                GenCore version 5.1.7
        Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on:   April 21, 2006, 12:58:49 ; Search time 47 Seconds
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                          550.585 Million cell updates/sec

Title:          US-10-664-421-1
Perfect score:  1670
Sequence:       1 MLLSKINSLAHLRAAPCNDL.........LLPQETAEIHLHSLSPGPSK 313

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters:        572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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        3:  /cgn2_6/ptodata/1/iaa/H_COMB.pep.*
        4:  /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
        5:  /cgn2_6/ptodata/1/iaa/RE_COMB.pep.*
        6:  /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
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2	1670	100.0	313	2	US-09-644-450-9	Sequence 9, Appli
3	1657	99.2	313	1	US-08-463-081B-26	Sequence 26, Appli
4	1657	99.2	313	1	US-08-461-379A-26	Sequence 26, Appli
5	1657	99.2	313	2	US-08-462-390B-26	Sequence 26, Appli
6	1657	99.2	313	2	US-08-463-074B-26	Sequence 26, Appli
7	1657	99.2	313	2	US-08-465-585C-26	Sequence 26, Appli
8	1657	99.2	313	2	US-08-652-446-26	Sequence 26, Appli
9	1636	98.0	313	2	US-09-237-543-8	Sequence 8, Appli
10	1636	98.0	313	2	US-09-644-450-8	Sequence 8, Appli
11	1582	94.7	313	2	US-09-237-543-7	Sequence 7, Appli
12	1582	94.7	313	2	US-09-644-450-7	Sequence 7, Appli
13	1296.5	77.6	257	1	US-07-857-224B-41	Sequence 41, Appli
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15	1133	67.8	326	2	US-09-644-450-2	Sequence 2, Appli
16	1128.5	67.6	455	2	US-09-237-543-5	Sequence 5, Appli
17	1128.5	67.6	455	2	US-09-644-450-5	Sequence 5, Appli
18	1105	66.2	323	2	US-09-237-543-6	Sequence 6, Appli
19	1105	66.2	323	2	US-09-644-450-6	Sequence 6, Appli
20	1079.5	64.6	254	2	US-09-237-543-4	Sequence 4, Appli
21	1079.5	64.6	254	2	US-09-644-450-4	Sequence 4, Appli
22	869.5	52.1	311	2	US-10-184-563-2	Sequence 2, Appli
23	869.5	52.1	372	2	US-09-949-016-7140	Sequence 7140, Ap
24	384.5	23.0	256	2	US-09-964-956-74	Sequence 74, Appl
25	376.5	22.5	776	2	US-09-523-849-34	Sequence 34, Appli
26	376	22.5	1101	2	US-09-770-170-8	Sequence 8, Appli
27	370.5	22.2	778	2	US-10-116-326-2	Sequence 2, Appli
28	370.5	22.2	778	2	US-10-003-690-2	Sequence 2, Appli
29	370.5	22.2	778	2	US-10-803-277-2	Sequence 2, Appli
30	368.5	22.1	630	2	US-10-355-975A-38	Sequence 38, Appl
31	368.5	22.1	631	2	US-10-579-664B-11	Sequence 11, Appl
32	368.5	22.1	631	2	US-10-355-975A-11	Sequence 11, Appl
33	367	22.0	1356	2	US-09-770-170-6	Sequence 6, Appli
34	364.5	21.8	256	2	US-09-964-956-72	Sequence 72, Appl
35	362.5	21.7	1323	2	US-09-770-170-2	Sequence 2, Appli
36	359	21.5	511	2	US-09-633-328B-4	Sequence 4, Appli
37	358.5	21.5	281	2	US-09-248-796A-20512	Sequence 20512, A
38	357.5	21.4	668	2	US-09-930-181-2	Sequence 2, Appli
39	357.5	21.4	668	2	US-10-054-579-2	Sequence 2, Appli
40	357	21.4	674	2	US-10-283-247-2	Sequence 2, Appli
41	357	21.4	512	2	US-09-633-328B-2	Sequence 2, Appli
42	353.5	21.2	674	2	US-10-283-247-7	Sequence 7, Appli
43	353.5	21.2	674	2	US-10-283-247-8	Sequence 8, Appli
44	349.5	20.9	722	2	US-08-817-832B-32	Sequence 32, Appli
45	348.5	20.9	722	2	US-09-984-890-4	Sequence 4, Appli

ALIGNMENTS

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RESULT 1
US-09-237-543-9
; Sequence 9, Application US/09237543A
; Patent No. 6143540
; GENERAL INFORMATION:
; APPLICANT: Kapeller, Rosana
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 035800/175631
; CURRENT APPLICATION NUMBER: US/09/237,543A
; CURRENT FILING DATE: 1999-01-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-237-543-9

  Query Match             100.0%;  Score 1670;  DB 2;  Length 313;
  Best Local Similarity   100.0%;  Pred. No. 7.5e-161;
  Matches  313;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy          61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
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Qy         121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
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Db         121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy         181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
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Db         181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy         241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
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Db         241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy         301 EIHLHSLSPGPSK 313
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Db         301 EIHLHSLSPGPSK 313

RESULT 2
US-09-644-450-9
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; Sequence 9, Application US/09644450
; Patent No. 6383791
; GENERAL INFORMATION:
; APPLICANT: Kapeller, Rosana
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 035800/175631
; CURRENT APPLICATION NUMBER: US/09/644,450
; CURRENT FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-644-450-9

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Query Match             100.0%;  Score 1670;  DB 2;  Length 313;
Best Local Similarity   100.0%;  Pred. No. 7.5e-161;
Matches  313; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
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Db   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy  61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
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Db  61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
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Db 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy 181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
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Db 181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy 241 PFEHDEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
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Db 241 PFEHDEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy 301 EIHLHSLSPGPSK 313
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Db 301 EIHLHSLSPGPSK 313
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RESULT 3
US-08-463-081B-26
; Sequence 26, Application US/08463081B
; Patent No. 5871960 5837487
; GENERAL INFORMATION:
; APPLICANT: Smith, Kendall A. & Beadling, Carol
; TITLE OF INVENTION: Nucleic Acids Encoding CR5 Polypeptide,
; TITLE OF INVENTION: Vector and Transformed Cell Thereof, and Expression Thereof
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
; STREET: 444 South Flower St. - Suite 1900
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0,
; SOFTWARE: Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,081B
; FILING DATE: 5-JUN-1995
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/104,736
; FILING DATE: 10-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/796,066
; FILING DATE: 20-NOV-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Viviana Amzel, Ph. D.
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: P66 38150 (DART-060)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 622-7700
; TELEFAX: (213) 489-4210
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 313 amino acids
; TYPE: amino acid
; STRANDEDNESS: n.a.
; TOPOLOGY: n.a.
; MOLECULE TYPE: peptide
US-08-463-081B-26

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Query Match             99.2%;  Score 1657;  DB 1;  Length 313;
Best Local Similarity   99.4%;  Pred. No. 1.6e-159;
Matches 311; Conservative   0; Mismatches   2; Indels   0; Gaps   0;

Qy   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
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Qy  61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
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Db  61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
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Db 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy 181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
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Db 241 PFEHDEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy 301 EIHLHSLSPGPSK 313
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Db 301 EIHLHSLSPGPSK 313
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RESULT 4
US-08-461-379A-26
; Sequence 26, Application US/08461379A
; Patent No. 5871961
; GENERAL INFORMATION:
; APPLICANT: Smith, Kendall A. & Beadling, Carol
; TITLE OF INVENTION: Nucleic Acids Encoding CR5 Polypeptide,
; TITLE OF INVENTION: Vector and Transformed Cell Thereof, and
; TITLE OF INVENTION: Expression Thereof
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; ADDRESSEE: .   (B) STREET:One Westlakes-Berwyn
; CITY: Valley Forge
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0,
; SOFTWARE: Version #1.25

CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/461,379A
  FILING DATE: 5-JUNE-1995
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: USSN 08/330,108; 08/104,736
  APPLICATION NUMBER: & 07/796,066
  FILING DATE: 27-OCT-1994; 10-AUG-1993 & 20-NOV-91
ATTORNEY/AGENT INFORMATION:
  NAME: Viviana Amzel, Ph.D.
  REGISTRATION NUMBER: 30,930
  REFERENCE/DOCKET NUMBER: DART-070
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (610)470-0700
  TELEFAX: (610)470-0701
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
  LENGTH: 313 amino acids
  TYPE: peptide
  STRANDEDNESS: n.a.
  TOPOLOGY: n.a.
  MOLECULE TYPE: peptide
US-08-461-379A-26

Query Match   99.2%;   Score 1657; DB 1; Length 313;
Best Local Similarity   99.4%;   Pred. No. 1.6e-159;
Matches 311;   Conservative   0;   Mismatches   2;   Indels   0;   Gaps   0;

Qy   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
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Db   1 MLLSKINSLAHLRARACNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
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Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCNCGVLHRDIKDENILIDLNRG 180
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Db 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCNCGVLHRDIKDENILIDLNRG 180

Qy 181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
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Db 181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy 241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
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Db 241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy 301 EIHLHSLSPGPSK 313
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Db 301 EIHLHSLSPGPSK 313

RESULT 5
US-08-462-390B-26
; Sequence 26, Application US/08462390B
; Patent No. 5882894
; GENERAL INFORMATION:
APPLICANT: Smith, K. A.; & Beadling, C.
TITLE OF INVENTION: Nucleic Acids Encoding CR8 Polypeptide, Vector and
TITLE OF INVENTION: Transformed Cell Thereof, and Expression Thereof
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
  ADDRESSEE: Ratner & Prestia
  ADDRESSEE: (B) STREET:One Westlakes-Berwyn
  CITY: Valley Forge
  STATE: Pennsylvania
  COUNTRY: USA
  ZIP: 19482
COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/462,390B
  FILING DATE: 5-JUNE-1995
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: USSN 08/330,108
  FILING DATE: 27-OCT-1994
  APPLICATION NUMBER: USSN 08/104,736
  FILING DATE: 10-AUG-1993
  APPLICATION NUMBER: USSN 07/796,066
  FILING DATE: 20-NOV-91
ATTORNEY/AGENT INFORMATION:
  NAME: Viviana Amzel, Ph. D.
  REGISTRATION NUMBER: 30,930
  REFERENCE/DOCKET NUMBER: DART-040
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (610)407-0700
  TELEFAX: (610)407-0701
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
  LENGTH: 313 amino acids
  TYPE: peptide
  STRANDEDNESS: n.a.
  TOPOLOGY: n.a.
  MOLECULE TYPE: peptide
US-08-462-390B-26

Query Match   99.2%;   Score 1657; DB 1; Length 313;
Best Local Similarity   99.4%;   Pred. No. 1.6e-159;
Matches 311;   Conservative   0;   Mismatches   2;   Indels   2;   Gaps   0;

Qy   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
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Db   1 MLLSKINSLAHLRARACNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
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Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCNCGVLHRDIKDENILIDLNRG 180
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Db 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCNCGVLHRDIKDENILIDLNRG 180

Qy 181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
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Db 181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy 241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
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Db 241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy 301 EIHLHSLSPGPSK 313
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Db 301 EIHLHSLSPGPSK 313

RESULT 6
US-08-463-074B-26
; Sequence 26, Application US/08463074B
; Patent No. 6020155
; GENERAL INFORMATION:
APPLICANT: Smith, Kendall A. & Beadling, Carol
TITLE OF INVENTION: Nucleic Acids Encoding CR1 Fusion Protein, Vector an
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
  ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
  ADDRESSEE: (B) STREET:
  CITY: Los Angeles   444 South Flower St. - Suite 190(
  STATE: California
  COUNTRY: USA
  ZIP: 90071
COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible

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;       OPERATING SYSTEM: PC-DOS/MS-DOS
;       SOFTWARE: PatentIn Release #1.0,
;       SOFTWARE: Version #1.25
;   CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/08/463,074B
;       FILING DATE: 5-JUN-1995
;   PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: US 08/104,736
;       FILING DATE: 10-AUG-1993
;   PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: US 07/796,066
;       FILING DATE: 20-NOV-91
;   ATTORNEY/AGENT INFORMATION:
;       NAME: Viviana Amzel, Ph. D.
;       REGISTRATION NUMBER: 30,930
;       REFERENCE/DOCKET NUMBER: P66 38143 (DART-020)
;   TELECOMMUNICATION INFORMATION:
;       TELEPHONE: (213) 622-7700
;       TELEFAX: (213) 489-4210
; INFORMATION FOR SEQ ID NO: 26:
;   SEQUENCE CHARACTERISTICS:
;       LENGTH: 313 amino acids
;       TYPE: peptide
;       STRANDEDNESS: n.a.
;       TOPOLOGY: n.a.
;   MOLECULE TYPE: peptide
US-08-463-074B-26

Query Match          99.2%;  Score 1657; DB 2; Length 313;
Best Local Similarity 99.4%; Pred. No. 1.6e-159;
Matches 311; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy    1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD  60
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Db    1 MLLSKINSLAHLRARACNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD  60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
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Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCNCGVLHRDIKDENILIDLNRG 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCNCGVLHRDIKDENILIDLNRG 180

Qy  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
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Db  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy  241 PFEHDEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
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Db  241 PFEHDEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy  301 EIHLHSLSPGPSK 313
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Db  301 EIHLHSLSPGPSK 313

RESULT 7
US-08-465-585C-26
; Sequence 26, Application US/08465585C
; Patent No. 6027914
; GENERAL INFORMATION:
;   APPLICANT: Smith, K. A.; & Beadling, C.
;   TITLE OF INVENTION: Nucleic Acids Encoding CR6 Polypeptide, Vecto
;   TITLE OF INVENTION: Transformed Cell Thereof, and Expression Thereof
;   NUMBER OF SEQUENCES: 35
;   CORRESPONDENCE ADDRESS:
;       ADDRESSEE: PRETTY,SCHROEDER & POPLAWSKI
;       ADDRESSE:          (B) STREET:       444South Flower St. - Suite 190
;       CITY: Los Angeles
;       STATE: Californiaa
;       COUNTRY: USA
;       ZIP: 900071
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;       COMPUTER READABLE FORM:
;       MEDIUM TYPE: Floppy disk
;       COMPUTER: IBM PC compatible
;       OPERATING SYSTEM: PC-DOS/MS-DOS
;       SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/08/465,585C
;       FILING DATE: 5-JUNE-1995
;   PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: USSN 08/330,108
;       FILING DATE: 27-OCT-1994
;       APPLICATION NUMBER: USSN 08/104,736
;       FILING DATE: 10-AUG-1993
;       APPLICATION NUMBER: USSN 07/796,066
;       FILING DATE: 20-NOV-1991
;   ATTORNEY/AGENT INFORMATION:
;       NAME: Viviana Amzel, Ph. D.
;       REGISTRATION NUMBER: 30,930
;       REFERENCE/DOCKET NUMBER: P66 38149 (DART-050)
;   TELECOMMUNICATION INFORMATION:
;       TELEPHONE: (213) 622-7700
;       TELEFAX: (213) 4894210
; INFORMATION FOR SEQ ID NO: 26:
;   SEQUENCE CHARACTERISTICS:
;       LENGTH: 313 amino acids
;       TYPE: peptide
;       STRANDEDNESS: n.a.
;       TOPOLOGY: n.a.
;   MOLECULE TYPE: peptide
US-08-465-585C-26

Query Match          99.2%;  Score 1657; DB 2; Length 313;
Best Local Similarity 99.4%; Pred. No. 1.6e-159;
Matches 311; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy    1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD  60
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Db    1 MLLSKINSLAHLRARACNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD  60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHCNCGVLHRDIKDENILIDLNRG 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHCNCGVLHRDIKDENILIDLNRG 180

Qy  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy  241 PFEHDEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 PFEHDEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy  301 EIHLHSLSPGPSK 313
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Db  301 EIHLHSLSPGPSK 313

RESULT 8
US-08-652-446-26
; Sequence 26, Application US/0852446
; Patent No. 6057427
; GENERAL INFORMATION:
;   APPLICANT: Smith, Kendall A. & Beadling, Carol
;   TITLE OF INVENTION: Nucleic Acids Encoding CR5
;   TITLE OF INVENTION: Polypeptide, Vector and Transformed Cell Thereof, and
;   TITLE OF INVENTION: Expression Thereof
;   NUMBER OF SEQUENCES: 38
;   CORRESPONDENCE ADDRESS:
;       ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
;       ADDRESSEE: .         (B) STREET:       444 South Flower St. - Suite 1900
```

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; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0,
;           Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,446
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP App. # 96921319.8
; FILING DATE: 5-JAN-1998
; APPLICATION NUMBER: PCT/US/96/09194
; FILING DATE: 5-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,108
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/463,074
; FILING DATE: 5-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/462,337
; FILING DATE: 5-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/462,390
; FILING DATE: 5-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/465,585
; FILING DATE: 5-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/463,081
; FILING DATE: 5-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/461,379
; FILING DATE: 5-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/739,523
; FILING DATE: 29-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Viviana Amzel, Ph. D.
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: FP66 40035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 622-7700
; TELEFAX: (213) 489-4210
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 313 amino acids
; TYPE: peptide
; STRANDEDNESS: n.a.
; TOPOLOGY: n.a.
; MOLECULE TYPE: peptide
US-08-652-446-26

Query Match             99.2%;  Score 1657;  DB 2;  Length 313;
Best Local Similarity   99.4%;  Pred. No. 1.6e-159;
Matches   311;  Conservative   0;  Mismatches   2;  Indels   0;  Gaps   0;

Qy    1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGFGSVYSGIRVSD 60
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Db    1 MLLSKINSLAHLRARACNDLHATKLAPGKEKEPLESQYQVGPLLGSGFGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
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Qy  181 ELKLIDFGSGALLKDTVYTDPDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 ELKLIDFGSGALLKDTVYTDPDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy  241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy  301 EIHLHSLSPGPSK 313
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Db  301 EIHLHSLSPGPSK 313


RESULT 9
US-09-237-543-8
; Sequence 8, Application US/09237543A
; Patent No. 6143540
; GENERAL INFORMATION:
; APPLICANT: Kapeller, Rosana
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 035800/175631
; CURRENT APPLICATION NUMBER: US/09/237,543A
; CURRENT FILING DATE: 1999-01-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-237-543-8

Query Match             98.0%;  Score 1636;  DB 2;  Length 313;
Best Local Similarity   97.1%;  Pred. No. 2.1e-157;
Matches   304;  Conservative   6;  Mismatches   3;  Indels   0;  Gaps   0;

Qy    1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGFGSVYSGIRVSD 60
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Db    1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGFGSVYSGIRVAD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy  181 ELKLIDFGSGALLKDTVYTDPDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
         |||||||||||||||||||:||||||||||||||||||||||||||||||||||||||
Db  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy  241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
         ||||||::|:||||||||||||||||||||||:||||||:|||||||||||||||||:||
Db  241 PFEHDEEIVKGQVFFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300

Qy  301 EIHLHSLSPGPSK 313
         |||||||||:|||
Db  301 EIHLHSLSPSPSK 313


RESULT 10
US-09-644-450-8
; Sequence 8, Application US/09644450
; Patent No. 6383791
; GENERAL INFORMATION:
; APPLICANT: Kapeller, Rosana
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
; TITLE OF INVENTION:  AND USES THEREOF
; FILE REFERENCE: 035800/175631
; CURRENT APPLICATION NUMBER: US/09/644,450
; CURRENT FILING DATE: 2000-08-23
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;   NUMBER OF SEQ ID NOS: 11
;   SOFTWARE: PatentIn Ver. 2.0
;   SEQ ID NO 8
;   LENGTH: 313
;   TYPE: PRT
;   ORGANISM: Rattus norvegicus
US-09-644-450-8

Query Match           98.0%;  Score 1636;  DB 2;  Length 313;
Best Local Similarity 97.1%;  Pred. No. 2.1e-157;
Matches 304;  Conservative   6;  Mismatches   3;  Indels   0;  Gaps   0;

Qy      1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGFGSVYSGIRVSD 60
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Db      1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGFGSVYSGIRVAD 60

Qy     61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy    121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy    181 ELKLIDFGSGALLKDTVYTDFDGTRVSYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 ELKLIDFGSGALLKDTVYTDFDGTRVSYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy    241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
            |||||||:|||||::|||||||||||||||||||||||:||||:|||||||||| |::| |
Db    241 PFEHDEEIVKGQVYFRQRQTVSSECQHLIRWCLSLRPSDRPSFEEIRNHPWMQGDLLPQATA 300

Qy    301 EIHLHSLSPGPSK 313
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Db    301 EIHLHSLSPSPSK 313
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Query Match           94.7%;  Score 1582;  DB 2;  Length 313;
Best Local Similarity 93.9%;  Pred. No. 6.2e-152;
Matches 294;  Conservative  10;  Mismatches   9;  Indels   0;  Gaps   0;

Qy      1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGFGSVYSGIRVSD 60
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Db      1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGFGSVYSGIRVAD 60

Qy     61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
            ||||||||||||||||||||||||||||||||||||||:|||||||||||||||||||||
Db     61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120

Qy    121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
            ||||||||||||||||||||||:|||||||||||||||||||||||||||||||||:|||
Db    121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180

Qy    181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
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Query Match           94.7%;  Score 1582;  DB 2;  Length 313;
Best Local Similarity 93.9%;  Pred. No. 6.2e-152;
Matches 294;  Conservative  10;  Mismatches   9;  Indels   0;  Gaps   0;

Qy      1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGFGSVYSGIRVSD 60
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Db      1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGFGSVYSGIRVAD 60

Qy     61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
            ||||||||||||||||||||||||||||||||||||||:|||||||||||||||||||||
Db     61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120

Qy    121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
            ||||||||||||||||||||||:||||:|||||||||||||||||||||||||||:|||
Db    121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180

Qy    181 ELKLIDFGSGALLKDTVYTDFDGTRVSYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
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Db    181 ELKLIDFGSGALLKDTVYTDFDGTRVSYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy    241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
            |||||||:|||||::|||||||||||||||||||||||:||||:|||||||||| |::||
Db    241 PFEHDEEIIKGQVFFRQRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300

Qy    301 EIHLHSLSPGPSK 313
            ||||||||| |||
Db    301 EIHLHSLSPGSSK 313
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;   COUNTRY: Switzerland
;   ZIP: (note: this is an international post code) CH-8092
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
;   COMPUTER: Apple Macintosh
;   OPERATING SYSTEM: Macintosh 7.0
;   SOFTWARE: Microsoft Word
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/07/857,224B
;   FILING DATE: 03/25/92
;   CLASSIFICATION: 436
;   PRIOR APPLICATION DATA: none
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (International) 41 1 632 2830
;   TELEFAX: (International) 41 1 262 2437
;   TELEX: none
;   INFORMATION FOR SEQ ID NO: 41:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 257
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE:
;   DESCRIPTION: protein
;   ORIGINAL SOURCE:
;   ORGANISM: rat
;   FEATURE: Protein kinase; Table 8 Column 46
;   PUBLICATION INFORMATION:
;   AUTHORS: Hanks, S. K.
;   AUTHORS: Quinn, A. M.
;   AUTHORS: Hunter, T.
;   TITLE: The protein kinase family
;   JOURNAL: Science
;   VOLUME: 241
;   PAGES: 42-52
;   DATE: 1988
US-07-857-224B-41
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Query Match             77.6%;  Score 1296.5;  DB 1;  Length 257;
Best Local Similarity   94.2%;  Pred. No. 4.1e-123;
Matches    242;  Conservative    9;  Mismatches    3;  Indels    3;  Gaps    2;

Qy   36 SQYQVGPLLGSGGFGSVYSGIRVSDNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKK 95
         |||||||||||||||||||||||| |||||||||||||||||||   |||||||||||||
Db    1 SQYQVGPLLGSGGFGSVYSGIRVADNLPVAIKHVEKDRISDWGE--NGTRVPMEVVLLKK 58

Qy   96 VSSGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELARSFFWQVLEAV 155
         |||:||||||||||||||||||||||||||||||||||||||||||:|||:|||||||||
Db   59 VSSDFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEDLARGFFWQVLEAV 118

Qy  156 RHCHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRY 215
         |||||||||||||||||||||| :||:|||||||||||||||||||||||||||||||||
Db  119 RHCHNCGVLHRDIKDENILIDLSRGEIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRY 178

Qy  216 HRYHGRSAAVWSLGILLYDMVCGDIPF-EHDEEIIRGQVFFRQRVSSECQHLIRWCLALR 274
         |||||||||||||||||||||||||| ||||||||:||||||| ||||||||:|:||:|
Db  179 HRYHGRSAAVWSLGILLYDMVCGDIPFDEHDEEIIKGQVFFRQVSSECQHLIKWCLSLR 238

Qy  275 PSDRPTFEEIQNHPWMQ 291
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Db  239 PSDRPSFEIRNHPWMQ 255
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RESULT 14
US-09-237-543-2
;   Sequence 2, Application US/09237543A
;   Patent No. 6143540
;   GENERAL INFORMATION:
;   APPLICANT: Kapeller, Rosana
;   TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
;   TITLE OF INVENTION: AND USES THEREOF
;   FILE REFERENCE: 035800/175631
;   CURRENT APPLICATION NUMBER: US/09/237,543A
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;   CURRENT FILING DATE: 1999-01-26
;   NUMBER OF SEQ ID NOS: 11
;   SOFTWARE: PatentIn Ver. 2.0
;   SEQ ID NO 2
;   LENGTH: 326
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-237-543-2
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Query Match             67.8%;  Score 1133;  DB 2;  Length 326;
Best Local Similarity   69.3%;  Pred. No. 2.1e-106;
Matches    219;  Conservative   35;  Mismatches   52;  Indels   10;  Gaps    7;

Qy    1 MLLSKINSLAHLRAAP--CNDLHATKLAPGK-EKEPLESQYQVGPLLGSGGFGSVYSGIR 57
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Db    1 MLLSKFGSLAHL-CGPGGVDHLPVKILQPAKADKESFEKAYQVGAVLGSGGFGTVYAGSR 59

Qy   58 VSDNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKV--SSGFSGVIRLLDWFERPDS 115
         ::|:|||||:|||  :|:::||  | |::|  ||:||:||   ||:|||||||||||||
Db   60 IADGLPVAVKHVVKERVTEWGSL-GGATVPLEVVLLRKVGAAGGARGVIRLLDWFERPDG 118

Qy  116 FVLILERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILI 175
         | |:||||||:||||||||||||| | ||| || ||| |||||:||| |||||||||:|
Db  119 FLLVLERPEPAQDLFDFITERGALDEPLARRFFAQVLAAVRHCHSCGVVHRDIKDENLLV 178

Qy  176 DLNRGELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDM 235
         ||:|||||||||||||||||||||||||||||||||||||||||||||:||||| ||||
Db  179 DLRSGELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSATVWSLGVLLYDM 238

Qy  236 VCGDIPFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWM--QDV 293
         ||||||| |:|:|||   ||:|:||:|||::|||| :|: | |::  :|:||: ||
Db  239 VCGDIPFEQDEEILRGRLLFRRRVSPECQQIRWCLSLRPSERPSLDQIAAHPWMLGADG 298

Qy  294 LLPQETAEIHLHSLSP 309
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Db  299 GAP-ESCDLRLCTLDP 313
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RESULT 15
US-09-644-450-2
;   Sequence 2, Application US/09644450
;   Patent No. 6383791
;   GENERAL INFORMATION:
;   APPLICANT: Kapeller, Rosana
;   TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
;   TITLE OF INVENTION: AND USES THEREOF
;   FILE REFERENCE: 035800/175631
;   CURRENT APPLICATION NUMBER: US/09/644,450
;   CURRENT FILING DATE: 2000-08-23
;   NUMBER OF SEQ ID NOS: 11
;   SOFTWARE: PatentIn Ver. 2.0
;   SEQ ID NO 2
;   LENGTH: 326
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-644-450-2
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Query Match             67.8%;  Score 1133;  DB 2;  Length 326;
Best Local Similarity   69.3%;  Pred. No. 2.1e-106;
Matches    219;  Conservative   35;  Mismatches   52;  Indels   10;  Gaps    7;

Qy    1 MLLSKINSLAHLRAAP--CNDLHATKLAPGK-EKEPLESQYQVGPLLGSGGFGSVYSGIR 57
         ||||| ||||        :||      |  |     |:||||| |||||||||| |: |
Db    1 MLLSKFGSLAHL-CGPGGVDHLPVKILQPAKADKESFEKAYQVGAVLGSGGFGTVYAGSR 59

Qy   58 VSDNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKV--SSGFSGVIRLLDWFERPDS 115
         ::|:|||||:|||  :|:::||  | |::|  ||:||:||   ||:|||||||||||||
Db   60 IADGLPVAVKHVVKERVTEWGSL-GGATVPLEVVLLRKVGAAGGARGVIRLLDWFERPDG 118

Qy  116 FVLILERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILI 175
         | |:||||||:||||||||||||| | ||| || ||| |||||:||| |||||||||:|
Db  119 FLLVLERPEPAQDLFDFITERGALDEPLARRFFAQVLAAVRHCHSCGVVHRDIKDENLLV 178
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Qy   176 DLNRGELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDM 235
          ||||||||||||||||||||||||||||||||||||||||||||||||| :||||
Db   179 DLRSGELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSATVWSLGVLLYDM 238

Qy   236 VCGDIPFEHDEBIIRGQVPFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWM--QDV 293
          |||||||| |||:|:: ||| ||| |||| |:: ::| |||| |
Db   239 VCGDIPFEQDEBILRGRLLFRRRVSPECQQLIRWCLSLRPSERPSLDQIAAHPWMLGADG 298

Qy   294 LLPQETAEIHLHSLSP 309
          |--|: :: :|| :|—|
Db   299 GAP-ESCDLRLCTLDP 313

Search completed: April 21, 2006, 13:00:11
Job time : 48 secs

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                    GenCore version 5.1.7
          Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on:    April 21, 2006, 12:54:19 ; Search time 228 Seconds
                              (without alignments)
                   968.554 Million cell updates/sec

Title:           US-10-664-421-1
Perfect score:   1670
Sequence:        1 MLLSKINSLAHLRAAPCNDL.........LLPQETABIHLHSLSPGPSK 313

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters:       2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       UniProt_05.80:*
                 1: uniprot_sprot:*
                 2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
```

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1670	100.0	313	1	P11309 PIM1_HUMAN	homo sapien
2	1670	100.0	313	2	Q5T7H7 Q5T7H7_HUMAN	homo sapien
3	1659	99.3	313	2	Q95lj0 PIM1_FELCA	felis silve
4	1656	99.2	313	1	Q9n0p9 PIM1_BOVIN	bos taurus
5	1636	98.0	313	1	P26794 PIM1_RAT	rattus norv
6	1587	95.0	313	2	Q8cfn8 Q8CFN8_MOUSE	mus musculu
7	1582	94.7	313	2	P06803 PIM1_MOUSE	mus musculu
8	1140	68.3	323	2	Q9pu85 PIM3_COTJA	coturnix co
9	1133	67.8	326	1	Q86v96 PIM3_HUMAN	homo sapien
10	1129.5	67.6	326	2	P58750 PIM3_MOUSE	mus musculu
11	1128.5	67.6	380	2	O70444 PIM3_RAT	rattus norv
12	1128.5	67.6	326	2	Q4v8m2 Q4V8M2_RAT	rattus norv
13	1116	66.8	325	2	Q811x8 Q811X8_MOUSE	mus musculu
14	1105	66.2	323	2	Q91822 PIM3_XENLA	xenopus lae
15	1101	65.9	318	2	Q66ii1 Q66II1_XENTR	xenopus tro
16	1092	65.4	337	2	Q5u489 Q5U489_XENLA	xenopus lae
17	1065	63.8	316	2	Q4stf0 Q4STF0_TETNG	tetraodon n
18	881.5	52.8	311	2	Q8r2p0 Q8R2P0_MOUSE	mus musculu
19	881.5	52.8	370	1	Q62070 PIM2_MOUSE	mus musculu
20	869.5	52.1	311	2	Q9p1w9 PIM2_HUMAN	homo sapien
21	854	51.1	310	2	Q7zvj5 Q7ZVJ5_BRARE	brachydanio
22	851	51.0	310	2	Q8jfw9 Q8JFW9_BRARE	brachydanio
23	846	50.7	310	1	Q9yhz5 PIM1_BRARE	brachydanio
24	844	50.5	310	2	Q6di52 Q6DI52_BRARE	brachydanio
25	799.5	47.9	288	2	Q4tdc2 Q4TDC2_TETNG	tetraodon n
26	716.5	42.9	221	2	Q8riz0 Q8RIZ0_MOUSE	mus musculu
27	626	37.5	500	2	Q61jb7 Q61JB7_CAEBR	caenorhabdi
28	617	36.9	441	2	Q20443 Q20443_CAEEL	caenorhabdi
29	497	29.8	566	2	Q61zz8 Q61ZZ8_CAEBR	caenorhabdi
30	486	29.1	378	2	Q8t3f1 Q8T3F1_CAEEL	caenorhabdi
31	486	29.1	566	2	Q17737 Q17737_CAEEL	caenorhabdi
32	440	26.3	270	2	Q5SPE4 Q5SPE4_BRARE	brachydanio
33	423	25.3	465	2	Q5SPF6 Q5SPF6_BRARE	brachydanio
34	421.5	25.2	134	2	Q6P2J9 Q6P2J9_HUMAN	homo sapien
35	421	25.2	416	2	Q4RFY6 Q4RFY6_TETNG	tetraodon n
36	412	24.7	281	2	Q5SV44 Q5SV44_BRARE	brachydanio
37	403	24.1	125	2	Q6Q2K5 Q6Q2K5_CANFA	canis famil
38	394.5	23.6	268	2	Q5SPP9 Q5SPP9_BRARE	brachydanio
39	391.5	23.4	578	2	Q5RH93 Q5RH93_BRARE	brachydanio
40	389.5	23.3	1383	1	Q8cee6 PASK_MOUSE	mus musculu
41	388	23.2	463	2	Q5RG24 Q5RG24_BRARE	brachydanio
42	388	23.2	465	2	Q5RG26 Q5RG26_BRARE	brachydanio
43	388	23.2	465	2	Q5TYR9 Q5TYR9_BRARE	brachydanio
44	388	23.2	1385	2	Q5PQT0 Q5PQT0_RAT	rattus norv
45	387	23.2	1107	2	Q6C310 Q6C310_YARLI	yarrowia li

ALIGNMENTS

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RESULT 1
PIM1_HUMAN
ID   PIM1_HUMAN     STANDARD;      PRT;    313 AA.
AC   P11309; Q96RG3;
DT   01-JUL-1989 (Rel. 11, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Proto-oncogene serine/threonine-protein kinase Pim-1 (EC 2.7.1.37).
GN   Name=PIM1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=90382681; PubMed=2205533; DOI=10.1016/0378-1119(90)90195-W;
RA   Reeves R., Spies G.A., Kiefer M., Barr P.J., Power M.;
RT   "Primary structure of the putative human oncogene, pim-1.";
RL   Gene 90:303-307(1990).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=87277423; PubMed=3475233; DOI=10.1016/0378-1119(87)90352-0;
RA   Zakut-Houri R., Hazum S., Givol D., Telerman A.;
RT   "The cDNA sequence and gene analysis of the human pim oncogene.";
RL   Gene 54:105-111(1987).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=88217305; PubMed=3329709;
RA   Domen J., von Lindern M., Hermans A., Breuer M., Grosveld G.,
RA   Berns A.;
RT   "Comparison of the human and mouse PIM-1 cDNAs: nucleotide sequence
RT   and immunological identification of the in vitro synthesized PIM-1
RT   protein.";
RL   Oncogene Res. 1:103-112(1987).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=88115604; PubMed=3429489;
RA   Meeker T.C., Nagarajan L., Ar-Rushdi A., Croce C.M.;
RT   "Cloning and characterization of the human PIM-1 gene: a putative
RT   oncogene related to the protein kinases.";
RL   J. Cell. Biochem. 35:105-112(1987).
RN   [5]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Kidney;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
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RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [6]
RP   NUCLEOTIDE SEQUENCE OF 1-202.
RX   MEDLINE=21354098; PubMed=11460166; DOI=10.1038/35085588;
RA   Pasqualucci L., Neumeister P., Goossens T., Nanjangud G.,
RA   Chaganti R.S.K., Kuppers R., Dalla-Favera R.;
RT   "Hypermutation of multiple proto-oncogenes in B-cell diffuse large-
RT   cell lymphomas.";
RL   Nature 412:341-346(2001).
RN   [7]
RP   CHARACTERIZATION.
RX   MEDLINE=88246418; PubMed=2837645;
RA   Telerman A., Amson R., Zakut-Houri R., Givol D.;
RT   "Identification of the human pim-1 gene product as a 33-kilodalton
RT   cytoplasmic protein with tyrosine kinase activity.";
RL   Mol. Cell. Biol. 8:1498-1503(1988).
RN   [8]
RP   FUNCTION.
RX   MEDLINE=20130009; PubMed=10664448; DOI=10.1016/S0014-5793(00)01105-4;
RA   Koike N., Maita H., Taira T., Ariga H., Iguchi-Ariga S.M.M.;
RT   "Identification of heterochromatin protein 1 (HP1) as a
RT   phosphorylation target by Pim-1 kinase and the effect of
RT   phosphorylation on the transcriptional repression function of HP1.";
RL   FEBS Lett. 467:17-21(2000).
RN   [9]
RP   SUBCELLULAR LOCATION.
RX   MEDLINE=22567470; PubMed=12680209;
RA   Ionov Y., Le X., Tunquist B.J., Sweetenham J., Sachs T., Ryder J.,
RA   Johnson T., Lilly M.B., Kraft A.S.;
RT   "Pim-1 protein kinase is nuclear in Burkitt's lymphoma: nuclear
RT   localization is necessary for its biologic effects.";
RL   Anticancer Res. 23:167-178(2003).
CC   -!- FUNCTION: Thought to play a role in signal transduction in blood
CC       cells. May affect the structure or silencing of chromatin by
CC       phosphorylating HP1 gamma/CBX3.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- SUBUNIT: Binds to RP9 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear.
CC   -!- TISSUE SPECIFICITY: Expressed primarily in cells of the
CC       hematopoietic and germ line lineages.
CC   -!- PTM: Autophosphorylated on tyrosine residues.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC       subfamily.
CC   -!- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
CC       WWW="http://www.infobiogen.fr/services/chromcancer/Genes/PIM1ID261.html".
CC
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC
DR   EMBL; M27903; AAA60090.1; -; Genomic_DNA.
DR   EMBL; M16750; AAA60089.1; -; mRNA.
DR   EMBL; M54915; AAA36447.1; -; mRNA.
DR   EMBL; M24779; AAA81553.1; -; mRNA.
DR   EMBL; BC020224; AAH20224.1; -; mRNA.
DR   EMBL; AF386792; AAK70871.1; -; Genomic_DNA.
DR   PIR; JU0327; TVHUP1.
DR   PDB; 1XQZ; X-ray; A=14-313.
DR   PDB; 1XR1; X-ray; A=14-313.
DR   PDB; 1XWS; X-ray; A=1-313.

DR   PDB; 1YHS; X-ray; A=33-305.
DR   PDB; 1YI3; X-ray; A=33-305.
DR   PDB; 1YI4; X-ray; A=33-305.
DR   PDB; 2BIK; X-ray; B=1-313.
DR   PDB; 2BIL; X-ray; B=1-313.
DR   Ensembl; ENSG00000137193; Homo sapiens.
DR   HGNC; HGNC:8986; PIM1.
DR   H-InvDB; HIX0005835; -.
DR   MIM; 164960;-.
DR   GO; GO:0005737; C:cytoplasm; TAS.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; TAS.
DR   GO; GO:0007275; P:development; TAS.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; TAS.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_Thr_pkin_AS.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   3D-structure; ATP-binding; Kinase; Nuclear protein;
KW   Nucleotide-binding; Phosphorylation; Proto-oncogene;
KW   Serine/threonine-protein kinase; Transferase.
FT   DOMAIN       38    290       Protein kinase.
FT   NP_BIND      44     52       ATP (By similarity).
FT   ACT_SITE    167    167       Proton acceptor (By similarity).
FT   BINDING      67     67       ATP (By similarity).
FT   CONFLICT     15     16       AP -> RA (in Ref. 2).
SQ   SEQUENCE   313 AA;  35686 MW;  35BA76D3668E69A3 CRC64;

Query Match             100.0%;  Score 1670;  DB 1;  Length 313;
Best Local Similarity   100.0%;  Pred. No. 7.2e-115;
Matches  313;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy         61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy        121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy        181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy        241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQQDVLLPQETA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQQDVLLPQETA 300

Qy        301 EIHLHSLSPGPSK 313
              |||||||||||||
Db        301 EIHLHSLSPGPSK 313


RESULT 2
Q5TH7_HUMAN
ID   Q5TH7_HUMAN  PRELIMINARY;      PRT;   313 AA.
AC   Q5TH7;
DT   01-FEB-2005 (TrEMBLrel. 29, Created)
DT   01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   Pim-1 oncogene (Proviral integration site 1).
GN   Name=PIM1; ORFNames=RP3-355M6.1-003;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
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RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Laird G.;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR   EMBL; AJ353579; CAI20316.1; -; Genomic_DNA.
     SMR; Q5T7H7; 32-308.
DR,  Ensembl; ENSG00000137193; Homo sapiens.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_Thr_pkin_AS.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   Pfam; PF00069; Pkinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Nucleotide-binding;
KW   Serine/threonine-protein kinase; Transferase.
SQ   SEQUENCE   313 AA;  35686 MW;  35BA76D3668B69A3 CRC64;

Query Match             100.0%;  Score 1670;  DB 2;  Length 313;
  Best Local Similarity   100.0%;  Pred. No. 7.2e-115;
  Matches  313;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy         61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy        121 ERREPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ERREPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy        181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy        241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy        301 EIHLHSLSPGPSK 313
              |||||||||||||
Db        301 EIHLHSLSPGPSK 313

RESULT 3
PIM1_FELCA
ID   PIM1_FELCA     STANDARD;      PRT;   313 AA.
AC   Q95LJ0;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Proto-oncogene serine/threonine-protein kinase pim-1 (EC 2.7.1.37).
GN   Name=PIM1;
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
OC   Felinae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Fujino Y., Satoh H., Hisasue M., Masuda K., Ohno K., Tsujimoto H.;
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RT   "The cDNA sequence of the feline pim-1 oncogene.";
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- SUBUNIT: Binds to RP9 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
CC   -!- PTM: Autophosphorylated (By similarity).
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC       subfamily.
CC   -----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   -----------------------------------------------------------------------
DR   EMBL; AB073748; BAB71752.1; -; mRNA.
DR   SMR; Q95LJ0; 32-308.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Nuclear protein; Nucleotide-binding;
KW   Phosphorylation; Proto-oncogene; Serine/threonine-protein kinase;
KW   Transferase.
FT   DOMAIN       38    290       Protein kinase.
FT   NP_BIND      44     52       ATP (By similarity).
FT   ACT_SITE    167    167       Proton acceptor (By similarity).
FT   BINDING      67     67       ATP (By similarity).
SQ   SEQUENCE   313 AA;  35686 MW;  COBE268D63B85967 CRC64;

Query Match             99.3%;  Score 1659;  DB 1;  Length 313;
  Best Local Similarity   99.0%;  Pred. No. 4.6e-114;
  Matches  310;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
              |||||||||||||:|||||||||||||||||||||||||||||||||||||||||||||:
Db          1 MLLSKINSLAHLRTAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60

Qy         61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy        121 ERREPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ERREPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy        181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy        241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy        301 EIHLHSLSPGPSK 313
              |||||||||||||
Db        301 EIHLHSLSPGPSK 313

RESULT 4
PIM1_BOVIN
ID   PIM1_BOVIN     STANDARD;      PRT;   313 AA.
AC   Q9N0P9;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Proto-oncogene serine/threonine-protein kinase pim-1 (EC 2.7.1.37).
GN   Name=PIM1;
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC   Pecora; Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RX   MEDLINE=21109090; PubMed=11182156; DOI=10.1016/S0165-2427(00)00259-2;
RA   Wang Z., Petersen K., Weaver M.S., Magnuson N.S.;
RT   "cDNA cloning, sequencing and characterization of bovine pim-1.";
RL   Vet. Immunol. Immunopathol. 78:177-195(2001).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- SUBUNIT: Binds to RP9 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
CC   -!- PTM: Autophosphorylated (By similarity).
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC       subfamily.
CC   ---------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------
DR   EMBL; AF259078; AAF67200.1; -; mRNA.
DR   HSSP; Q63450; 1A06.
DR   SMR; Q9NOP9; 32-308.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Nuclear protein; Nucleotide-binding;
KW   Phosphorylation; Proto-oncogene; Serine/threonine-protein kinase;
KW   Transferase.
FT   DOMAIN        38    290       Protein kinase.
FT   NP_BIND       44     52       ATP (By similarity).
FT   ACT_SITE     167    167       Proton acceptor (By similarity).
FT   BINDING       67     67       ATP (By similarity).
SQ   SEQUENCE    313 AA;   35630 MW;  9EF40229A847AD47 CRC64;

Query Match             99.2%;  Score 1656;  DB 1;  Length 313;
Best Local Similarity   98.7%;  Pred. No. 7.7e-114;
Matches   309;  Conservative   4;  Mismatches   0;  Indels   0;  Gaps   0;

Qy     1  MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD   60
          ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||: 
Db     1  MLLSKINSLAHLRAAPCSDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD   60

Qy    61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL  120

Qy   121  ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG  180
          ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db   121  ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHDCGVLHRDIKDENILIDLNRG  180

Qy   181  ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI  240

Qy   241  PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA  300
          |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  PFEHDEEIVRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA  300

Qy   301  EIHLHSLSPGPSK  313
          |||||||||||||
Db   301  EIHLHSLSPGPSK  313
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AC   P26794;
DT   01-AUG-1992 (Rel. 23, Created)
DT   01-AUG-1992 (Rel. 23, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Proto-oncogene serine/threonine-protein kinase Pim-1 (EC 2.7.1.37).
GN   Name=Pim1; Synonyms=Pim-1;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Sprague-Dawley; TISSUE=Testis;
RX   MEDLINE=92319652; PubMed=1620615;
RA   Wingett D., Reeves R., Magnuson N.S.;
RT   "Characterization of the testes-specific pim-1 transcript in rat.";
RL   Nucleic Acids Res. 20:3183-3189(1992).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- SUBUNIT: Binds to RP9 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
CC   -!- PTM: Autophosphorylated (By similarity).
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC       subfamily.
CC   ---------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------
DR   EMBL; X63675; CAA45214.1; -; mRNA.
DR   PIR; S26298; S26298.
DR   SMR; P26794; 32-308.
DR   Ensembl; ENSRNOG00000000529; Rattus norvegicus.
DR   RGD; 3330; Pim1.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Nuclear protein; Nucleotide-binding;
KW   Phosphorylation; Proto-oncogene; Serine/threonine-protein kinase;
KW   Transferase.
FT   DOMAIN        38    290       Protein kinase.
FT   NP_BIND       44     52       ATP (By similarity).
FT   ACT_SITE     167    167       Proton acceptor (By similarity).
FT   BINDING       67     67       ATP (By similarity).
SQ   SEQUENCE    313 AA;   35631 MW;  D5757DA9F1821BF9 CRC64;

Query Match             98.0%;  Score 1636;  DB 1;  Length 313;
Best Local Similarity   97.1%;  Pred. No. 2.3e-112;
Matches   304;  Conservative   6;  Mismatches   3;  Indels   0;  Gaps   0;

Qy     1  MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD   60
          ||||||||||||||||:||||||:|||||||||||||||||||||||||||||||||:
Db     1  MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD   60

Qy    61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL  120

Qy   121  ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG  180

Qy   181  ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI  240

Qy   241  PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA  300
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RESULT 5
PIM1_RAT
ID   PIM1_RAT     STANDARD;     PRT;    313 AA.
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Db        241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
              ||||||::||:||||||||||||||||||||||||||||||||||||||||||||||||||

Qy        301 EIHLHSLSPGPSK 313
              |||||:|||||||
Db        301 EIHLHSLSPSPSK 313


RESULT 6
Q8CFN8 MOUSE
ID   Q8CFN8_MOUSE PRELIMINARY;       PRT;   313 AA.
AC   Q8CFN8;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Proviral integration site 1.
GN   Name=Pim1;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6; TISSUE=Brain, and Eye;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Eye;
RA   Strausberg R.;
RL   Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6; TISSUE=Brain;
RA   Strausberg R.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6; TISSUE=Brain;
RA   Strausberg R.;
RL   Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR   EMBL; BC042885; AAH42885.1; -; mRNA.
DR   EMBL; BC053019; AAH53019.1; -; mRNA.
DR   EMBL; BC055316; AAH55316.1; -; mRNA.
DR   SMR; Q8CFN8; 32-308.
DR   Ensembl; ENSMUSG00000024014; Mus musculus.
DR   MGI; MGI:97584; Pim1.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Nucleotide-binding;
KW   Serine/threonine-protein kinase; Transferase.
SQ   SEQUENCE   313 AA;  35451 MW;  1294F16A03B7C7D7 CRC64;

Query Match          95.0%;  Score 1587;  DB 2;  Length 313;
Best Local Similarity  94.2%;  Pred. No. 9.3e-109;
Matches  295;  Conservative  10;  Mismatches  8;  Indels  0;  Gaps  0;

Qy     1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||:||
Db     1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60

Qy    61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120

Qy   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180

Qy   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
           |:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy   241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
           |||||||:||:||||||||||||||||||||:||||||::||||:|||||||||||:
Db   241 PFEHDEEIIKGQVFFRQTVSSDRPSFEEIRNHPWMQGDLLPQAAS 300

Qy   301 EIHLHSLSPGPSK 313
           |||||:|||
Db   301 EIHLHSLSPGSSK 313


RESULT 7
PIM1_MOUSE
ID   PIM1_MOUSE      STANDARD;      PRT;   313 AA.
AC   P06803;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Proto-oncogene serine/threonine-protein kinase Pim-1 (EC 2.7.1.37).
GN   Name=Pim1; Synonyms=Pim-1;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=86272109; PubMed=3015420; DOI=10.1016/0092-8674(86)90886-X;
RA   Selten G., Cuypers H.T., Boelens W., Robanus-Maandag E., Verbeek J.,
RA   Domen J., van Beveren C., Berns A.;
RT   "The primary structure of the putative oncogene pim shows extensive
RT   homology with protein kinases.";
RL   Cell 46:603-611 (1986).
RN   [2]
RP   INTERACTION WITH RP9.
RX   MEDLINE=20389540; PubMed=10931201;
RA   Maita H., Harada Y., Nagakubo D., Kitaura H., Ikeda M., Tamai K.,
RA   Takahashi K., Ariga H., Iguchi-Ariga S.M.M.;
RT   "PAP-1, a novel target protein of phosphorylation by Pim-1 kinase.";
RL   Eur. J. Biochem. 267:5168-5178 (2000).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- SUBUNIT: Binds to RP9.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
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CC   -!- PTM: Autophosphorylated (By similarity).
CC   -!- DISEASE: Frequently activated by provirus insertion in murine
CC       leukemia virus-induced T-cell lymphomas.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC       subfamily.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   EMBL; M13995; AAA39930.1; -; Genomic_DNA.
DR   PIR; A24169; TVMSP1.
DR   HSSP; Q63450; 1A06.
DR   SMR; P06803; 32-308.
DR   Ensembl; ENSMUSG00000024014; Mus musculus.
DR   MGI; MGI:97584; Pim1.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Nuclear protein; Nucleotide-binding;
KW   Phosphorylation; Proto-oncogene; Serine/threonine-protein kinase;
KW   Transferase.
FT   DOMAIN       38    290       Protein kinase.
FT   NP_BIND      44     52       ATP (By similarity).
FT   ACT_SITE    167    167       Proton acceptor (By similarity).
FT   BINDING      67     67       ATP (By similarity).
SQ   SEQUENCE   313 AA;  35537 MW;  79F4779E9DCBDC16 CRC64;

Query Match             94.7%;  Score 1582;  DB 1;  Length 313;
Best Local Similarity   93.9%;  Pred. No. 2.2e-108;
        Matches  294;  Conservative   10;  Mismatches    9;  Indels    0;  Gaps    0;

Qy      1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60

Qy     61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120

Qy    121 ERPEPVQDLFDFITERGALQEELARSFFWQLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
          |||||||||||||||||||||||:||| |||||||||||||||||||||||||||:|
Db    121 ERPEPVQDLFDFITERGALQEDLARGFFWQLEAVRHCHNCGVLHRDIKDENILIDLSRG 180

Qy    181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy    241 PFEHDEIIRGQVFFRQRVSSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
          |||||||:||||||||||||||||||||:|||||||||||||||||| |||||:||
Db    241 PFEHDEIIKGQVFFRQRQTVSSECQHLIRWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300

Qy    301 EIHLHSLSPGPSK 313
          ||||||||||| ||
Db-   301 EIHLHSLSPGSSK 313

RESULT 8
PIM3_COTJA
ID   PIM3_COTJA    STANDARD;      PRT;   323 AA.
AC   Q9PU05;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Serine/threonine-protein kinase Pim-3 (EC 2.7.1.37) (qpim).
GN   Name=PIM3; Synonyms=PIM-3;
OS   Coturnix coturnix japonica (Japanese quail).
```

```
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Coturnix.
OX   NCBI_TaxID=93934;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=20180111; PubMed=10713710; DOI=10.1038/sj.onc.1203355;
RA   Eichmann A., Yuan L., Breant C., Alitalo K., Koskinen P.J.;
RT   "Developmental expression of Pim kinases suggests functions also
RT   outside of the hematopoietic system.";
RL   Oncogene 19:1215-1224 (2000).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- PTM: Autophosphorylated.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC       subfamily.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   EMBL; AJ130845; CAB62386.1; -; mRNA.
DR   HSSP; Q63450; 1A06.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Nucleotide-binding; Phosphorylation;
KW   Serine/threonine-protein kinase; Transferase.
FT   DOMAIN       40    291       Protein kinase.
FT   NP_BIND      46     54       ATP (By similarity).
FT   ACT_SITE    168    168       Proton acceptor (By similarity).
FT   BINDING      69     69       ATP (By similarity).
SQ   SEQUENCE   323 AA;  36597 MW;  E2A4FA20B6F6396C CRC64;

Query Match             68.3%;  Score 1140;  DB 1;  Length 323;
Best Local Similarity   67.4%;  Pred. No. 8e-76;
        Matches  209;  Conservative   45;  Mismatches   52;  Indels    4;  Gaps    3;

Qy      1 MLLSKINSLAHLRAAPCNDLHATKLAP--GKEKEPLESQYQVGPLLGSGGFGSVYSGIRV 58
          ||||  ||| |||:       |  :  :::   : : |:::||||:||  :|  |:||||||
Db      1 MLLSKFGSLAHICSPASMDHLPVKILPPVKVEKEPFDKVYQVGVSVLGVGSGFGTVYAGSRT 60

Qy     59 SDNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVL 118
          :| |||::|.:.:.|:||      :| |::  :: :|::|||||:::::::
Db     61 ADGLPVAVKHVVKERVTEWGTI-GGVMVPLEIVLLKKVSSGFRGVIKLLDWYERPDGFLI 119

Qy    119 ILERPEPVQDLFDFITERGALQEELARSFFWQLEAVRHCHNCGVLHRDIKDENILIDLN 178
          :::||| |:||:|||:|:|||:|::||  :::||||||| : |||||||||||:||:||:
Db    120 VMERPELVKDLFDFITEKGALDEDTARGFFRQVLEAVRHCYCGCGVVHRDIKDENLLVDLR 179

Qy    179 RGELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCG 238
          .|| |||||||||||||:||||||||||||||||||||||||||||:::::||:||||||
Db    180 TGELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSATWSLGVLLYDMVCG 239

Qy    239 DIPFEHDEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWM-QDVLLPQ 297
          ||||| :||:||::::||||:::||:||:|||:::|:|||| :::|::.:|: .::
Db    240 DIPFEQDEILRGRLYFRRRISPECQQLIKWCLSLRPSDRPTLEQIFDRQWMHKSEVVKS 299

Qy    298 ETAEIHLHSL 307
          :|::|:|:||
Db    300 EDCDIRLRTL 309

RESULT 9
PIM3_HUMAN
ID   PIM3_HUMAN    STANDARD;      PRT;   326 AA.
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AC   Q86V86; Q68BM2;
DT   29-MAR-2004 (Rel. 43, Created)
DT   29-MAR-2004 (Rel. 43, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Serine/threonine-protein kinase Pim-3 (EC 2.7.1.37).
GN   Name=PIM3;
OS   Homo sapiens (Human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA], FUNCTION, AND TISSUE SPECIFICITY.
RC   TISSUE=Liver;
RX   PubMed=15540201; DOI=10.1002/ijc.20719;
RA   Fujii C., Nakamoto Y., Lu P., Tsuneyama K., Popivanova B.K.,
RA   Kaneko S., Mukaida N.;
RT   "Aberrant expression of serine/threonine kinase Pim-3 in
RT   hepatocellular carcinoma development and its role in the proliferation
RT   of human hepatoma cell lines.";
RL   Int. J. Cancer 114:209-218(2005).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Lymph;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [3]
RP   IDENTIFICATION FROM ESTS.
RX   MEDLINE=22682943; PubMed=12798037; DOI=10.1016/S1476-9271(02)00095-6;
RA   Chichester C., Nikitin F., Ravarini J.-C., Lisacek F.;
RT   "Consistency checks for characterizing protein forms.";
RL   Comput. Biol. Chem. 27:29-35(2003).
CC   -!- FUNCTION: May be involved in cell cycle progression and anti-
CC       apoptosis process. Implicated in proliferation of human hepatoma
CC       cell lines.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- TISSUE SPECIFICITY: Widely expressed. No expression in colon,
CC       thymus, and small intestine. Expressed in human hepatoma cell
CC       lines but not in normal liver tissues.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC       subfamily.
CC   --------------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics  and the EMBL outstation -
CC   the European Bioinformatics Institute.  There are no  restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   --------------------------------------------------------------------------
DR   EMBL; AB114795; BAD42438.1; -; mRNA.
DR   EMBL; BC052239; -; NOT_ANNOTATED_CDS; mRNA.
DR   Ensembl; ENSG00000198355; Homo sapiens.
DR   HGNC; HGNC:19310; PIM3.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_Thr_pkin_AS.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Nucleotide-Binding; Phosphorylation;
KW   Serine/threonine-protein kinase; Transferase.
FT   DOMAIN        40    293       Protein kinase.
FT   NP_BIND       46     54       ATP (By similarity).
FT   ACT_SITE     170    170       Proton acceptor (By similarity).
FT   BINDING       69     69       ATP (By similarity).
SQ   SEQUENCE   326 AA;  35863 MW;  41FD9DD2467A162 CRC64;
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Query Match             67.8%;  Score 1133;  DB 1;  Length 326;
Best Local Similarity   69.3%;  Pred. No. 2.6e-75;
Matches  219;  Conservative  35;  Mismatches  52;  Indels  10;  Gaps  7;

Qy          1 MLLSKINSLAHLRAAP--CNDLHATKLAPGK-EKEPLESQYQVGPLLGSGGFGSVYSGIR  57
              |||||  ||||| :|||   :    |  | :  | |||||::|| |:|:|| ||||||||:|
Db          1 MLLSKFGSLAHL-CGPGGVDHLPVKILQPAKADKESFEKAYQVGAVLGSGGFGTVYAGSR  59

Qy         58 VSDNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKV--SSGFSGVIRLLDWFERPDS 115
              ::|| |||||:|| |::|||| ||||||||||| |:||   ::|:|| |||||||||||
Db         60 IADGLPVAVKHVVKERVTEWGSL-GGATVPLEVLLRKVGAAGGARGVIRLLDWFERPDG 118

Qy        116 FVLILERPEPVQDLFDFITERGALQELARSFFWQVLEAVRHCNCCVLHRDIKDENLI 175
              |:|:|||||| ||||||||||||||:|||||||||||||||::| :||||||||:|
Db        119 FLVLERPEPAQDLFDFITERGALDEPLARRFFAQVLAAVRHCHSCGVVHRDIKDENLLV 178

Qy        176 DLNRGELKLIDFGSGALLKDTVYTPDFGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDM 235
              || | ||||||||||||||||||||||||||||||||||||||||:|| |||| :| ||
Db        179 DLRSGELKLIDFGSGALLKDTVYTPDFGTRVYSPPEWIRYHRYHGRSATVWSLGVLLYDM 238

Qy        236 VCGDIPFEHDEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEIQNHPWM--QDV 293
              |||||||: |||||:||||| ||  | |:|||||| |:||||||| |||:| | :| : ||
Db        239 VCGDIPFEQDEILRGRLLFRRRVSPECQQLIRWCLSLRPSRPSLDQIAAHPWMLGADG 298

Qy        294 LLPQETAEIHLHSLSP 309
              ||| ||  | | ::||
Db        299 GAP-SCCDLRLCTLDP 313
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RESULT 10
PIM3_MOUSE
ID   PIM3_MOUSE     STANDARD;     PRT;     326 AA.
AC   P58750;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Serine/threonine-protein kinase Pim-3 (EC 2.7.1.37).
GN   Name=Pim3;
OS   Mus musculus (Mouse)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   STRAIN=FVB/N; TISSUE=Colon, and Salivary gland;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
```

RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC   subfamily.
CC   --
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   --
DR   EMBL; BC017621; AAH17621.1; -; mRNA.
DR   EMBL; BC026633; AAH26633.1; -; mRNA.
DR   HSSP; Q03656; 1HOW.
DR   Ensembl; ENSMUSG00000035828; Mus musculus.
DR   MGI; MGI:1355297; Pim3.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Nucleotide-binding; Phosphorylation;
KW   Serine/threonine-protein kinase; Transferase.
FT   DOMAIN   40   293   Protein kinase.
FT   NP_BIND   46   54   ATP (By similarity).
FT   ACT_SITE   170   170   Proton acceptor (By similarity).
FT   BINDING   69   69   ATP (By similarity).
SQ   SEQUENCE   326 AA; 35970 MW; DD68CBF4635481E CRC64;

Query Match   67.6%; Score 1129.5; DB 1; Length 326;
Best Local Similarity   72.2%; Pred. No. 4.8e-75;
Matches 213; Conservative 31; Mismatches 44; Indels 7; Gaps 5;

Qy   1 MLLSKINSLAHLRAAP--CNDLHATKLAPGK-EKEPLESOYQVGPLLGSGGFGSVYSGIR 57
Db   1 MLLSKFGSLAHL-CGPGGVDHLPVKILQPAKADKESFEKVYQVGAVLGSGFGTVYAGSR 59

Qy   58 VSDNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLKKV--SSGFSGVIRLLDWFERPDS 115
Db   60 IADGLPVAVKHVVKERVTEWGSL-GGVAVPLEVVLLRKVGAAGARGVIRLLDWFERPDG 118

Qy 116 FVLILERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHCGVLHRDIKDENILI 175
Db 119 FLLVLERPEPAQDLFDFITERGALDEPLARRFFAQVLAAVRHCHNCGVVHRDIKDENLLV 178

Qy 176 DLNRGELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYRYHRYHGRSAAVWSLGILLYDM 235
Db 179 DLRSGELKLIDFGSGSAVLKDTVYTDFDGTRVYSPPEWIRYRYHRYHGRSATVWSLGVLLYDM 238

Qy 236 VCGDIPFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWM 290
Db 239 VCGDIPFEQDEEILRGRLFPRRRVSPECQQLIEWCLSLRPSERPSLDQIAAHPWM 293

RESULT 11
PIM3_RAT
ID   PIM3_RAT   STANDARD;   PRT;   326 AA.
AC   O70444;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Serine/threonine-protein kinase Pim-3 (EC 2.7.1.37) (Protein kinase
DE   Kid-1) (Kinase induced by depolarization).

GN   Name=Pim3; Synonyms=Kid1;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Sprague-Dawley;
RA   Konietzko U., Kuhl D.;
RT   "Pim-3 is a member of the pim kinase family.";
RL   Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE, AND CHARACTERIZATION.
RX   MEDLINE=98298176; PubMed=9632723; DOI=10.1074/jbc.273.26.16535;
RA   Feldman J.D., Vician L., Crispino M., Tocco G., Marcheselli V.L.,
RA   Bazan N.G., Baudry M., Herschman H.R.;
RT   "KID-1, a protein kinase induced by depolarization in brain.";
RL   J. Biol. Chem. 273:16535-16543(1998).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- TISSUE SPECIFICITY: Present in a number of unstimulated tissues,
CC   including brain.
CC   -!- INDUCTION: By membrane depolarization or forskolin.
CC   -!- PTM: Autophosphorylated.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC   subfamily.
CC   --
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   --
DR   EMBL; AF086624; AAC68900.1; ALT_INIT; mRNA.
DR   EMBL; AF057026; AAC36065.1; -; mRNA.
DR   HSSP; Q03656; 1HOW.
DR   RGD; 620462; Pim3.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IDA.
DR   GO; GO:0016572; P:histone phosphorylation; IDA.
DR   GO; GO:0046777; P:autophosphorylation; IDA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Nucleotide-binding; Phosphorylation;
KW   Serine/threonine-protein kinase; Transferase.
FT   DOMAIN   40   293   Protein kinase.
FT   NP_BIND   46   54   ATP (By similarity).
FT   ACT_SITE   170   170   Proton acceptor (By similarity).
FT   BINDING   69   69   ATP (By similarity).
SQ   SEQUENCE   326 AA; 36002 MW; DD6C9BF4635F851E CRC64;

Query Match   67.6%; Score 1128.5; DB 1; Length 326;
Best Local Similarity   72.2%; Pred. No. 5.7e-75;
Matches 213; Conservative 31; Mismatches 44; Indels 7; Gaps 5;

Qy   1 MLLSKINSLAHLRAAP--CNDLHATKLAPGK-EKEPLESOYQVGPLLGSGGFGSVYSGIR 57
Db   1 MLLSKFGSLAHL-CGPGGVDHLPVKILQPAKADKESFEKVYQVGAVLGSGFGTVYAGSR 59

Qy   58 VSDNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLKKV--SSGFSGVIRLLDWFERPDS 115
Db   60 IADGLPVAVKHVVKERVTEWGSL-GGVAVPLEVVLLRKVGAAGARGVIRLLDWFERPDG 118

Qy 116 FVLILERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHCGVLHRDIKDENILI 175
Db 119 FLLVLERPEPAQDLFDFITERGALDEPLARRFFAQVLAAVRHCHNCGVVHRDIKDENLLV 178

Qy   176   DLNRGELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDM   235
             ||||| |||||||||||| ||| |||||||||||||||||||||||||:||| ||||||
Db   179   DLRSGELKLIDFGSGAVLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSATVWSLGVLLYDM   238

Qy   236   VCGDIPFEHDEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWM   290
             ||||||| |:||||||||||||:|::: || || |||| || : ||||
Db   239   VCGDIPFEQDEEILRGRLFFRRRVSPECQQLIEWCLSLRPSERPSLDQIAAHPWM   293

RESULT 12
Q4V8M2_RAT
ID   Q4V8M2_RAT   PRELIMINARY;   PRT;   380 AA.
AC   Q4V8M2;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Hypothetical protein (Fragment).
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Placenta;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Placenta;
RG   NIH MGC Project;
RL   Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR   EMBL; BC097317; AAH97317.1; -; mRNA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Hypothetical protein; Kinase; Nucleotide-binding;
KW   Serine/threonine-protein kinase; Transferase.
FT   NON_TER   1   1
SQ   SEQUENCE   380 AA;   41568 MW; F82BE850DD71346 CRC64;

Query Match   67.6%; Score 1128.5; DB 2; Length 380;
Best Local Similarity   72.2%; Pred. No. 6.8e-75;
Matches 213; Conservative 31; Mismatches 44; Indels 7; Gaps 5;

Qy   1   MLLSKINSLAHLRAAP--CNDLHATKLAPGK-EKEPLESQYQVGPLLGSGGGFGSVYSGIR   57
             ||||| || ||||| ||||||||||| |||||||||||||||||||||||||||
Db   1   MLLSKFGSLAHL-CGPGGVDHLPVKILQPAKADKESFEKVYQVGAVLGSGGFGTVYAGSR   113

Qy   58   VSDNLPVAIKVEKDRISDWGELPNGTRVPMEVVLLKKV--SSGFSGVIRLLDWFERPDS   115
             :::|||||||::|::|:: || || || |||| || || ||||||||
Db   114   IADGLPVAVKHVVKERVTEWGSL-GGMAVPLEVVLLRKVGAAGGARGVIRLLDWFERPDG   172

Qy   116   FVLILERPEPVQDLFDFITERGALQELARSFFWQVLEAVRHCHNCGVLHRDIKDENILI   175
             |:||||||||||||||||||||||||||| |||| ||||||||||||||||||||||
Db   173   FLLVLERPEPAQDLFDFITERGALDEPLARRFFAQVLAAVRHCHNCGVVHRDIKDENLLV   232

Qy   176   DLNRGELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDM   235
             ||||| |||||||||||| ||| |||||||||||||||||||||||||:||| ||||||
Db   233   DLRSGELKLIDFGSGAVLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSATVWSLGVLLYDM   292

Qy   236   VCGDIPFEHDEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWM   290
             ||||||| |:||||||||||||:|::: || || |||| || : ||||
Db   293   VCGDIPFEQDEEILRGRLFFRRRVSPECQQLIEWCLSLRPSERPSLDQIAAHPWM   347

RESULT 13
Q81IX8_MOUSE
ID   Q81IX8_MOUSE PRELIMINARY;   PRT;   325 AA.
AC   Q81IX8;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   KID1.
GN   Name=Pim3; Synonyms=Kid1;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Yu L.;
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR   EMBL; AY026239; AAK16606.1; -; mRNA.
DR   HSSP; Q03556; 1Q99.
DR   SMR; Q81IX8; 36-292.
DR   MGI; MGI:1355297; Pim3.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Nucleotide-binding;
KW   Serine/threonine-protein kinase; Transferase.
SQ   SEQUENCE   325 AA; 35931 MW; 77DEF8E20F41E3F4 CRC64;

Query Match   66.8%; Score 1116; DB 2; Length 325;
Best Local Similarity   71.9%; Pred. No. 4.7e-74;
Matches 212; Conservative 32; Mismatches 43; Indels 8; Gaps 6;

Qy   1   MLLSKINSLAHLRAAP--CNDLHATKLAPGK-EKEPLESQYQVGPLLGSGGGFGSVYSGIR   57
             ||||| || ||||| ||||||||||| |||||||||||||||||||||||||||
Db   1   MLLSKFGSLAHL-CGPGGVDHLPVKILQPAKADKESFEKVYQVGAVLGSGGFGTVYAGSR   57

Qy   58   VSDNLPVAIKVEKDRISDWGELPNGTRVPMEVVLLKKV--SSGFSGVIRLLDWFERPDS   115
             :::|||||||::|::|:: || || || |||| || || ||||||||
Db   60   IADGLPVAVKHVVKERVTEWGSL-GGVAVPLEVVLLRKVGAAGGARGVIRLLDWFERPDG   118

Qy   116   FVLILERPEPVQDLFDFITERGALQELARSFFWQVLEAVRHCHNCGVLHRDIKDENILI   175
             |:||||||||||||||||||||||||||| |||| ||||||||||||||||||||||
Db   119   FLLVLERPEPAQDLFDFITERGALDEPLARRFFAQVLAAVRHCHNCGVVHRDIKDENLLV   178

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Qy    55  GIRVSDNLPVAIKHVEKDRISDWGELPNGTRVSPMEVVLLKKVSSGPSGVIRLLDWFERPD 114
              |||| |||||:|||||:|  |  |: |: ||||| ||: ||||||||| | :|||||| ||||
Db    57  DSRIADGQPVAVKHVAKERVTEWGTL-NGVMVPLEIVLLKKVPTAFRGVINLLDWYERPD 115

Qy   115  SFVLILERPPVQDLFDFITERGALQEELARSFFWQVLEAVRHCNCGVLHRDIKDENIL 174
              ||| ||||| |||: ||:|||:| :|||: | |||||||||||||||||||||:|:|||:|
Db   116  AFLIVMERPEPVKDLFDYITEKGPLDEDTARGFFRQVLEAVRHCNCGVVHRDIKDENLL 175

Qy   175  IDLNRGELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYD 234
              : ||||||||||||||||||| |||||||||||||||||||||:||||||  |||||||||
Db   176  VDTRNGELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSATVWSLGVLLYD 235

Qy   235  MVCGDIPFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWM-QDV 293
              || ||||||  || |||||| | |||| |  ||||||||| |||||||  ||||||| | |
Db   236  MVYGDIPFEQDEEIVRVLCFRRRISTECQQLIKWCLSLRPSDRPTLEQIFDHPWMCKCD 295

Qy   294  LLPQETAEIHLHSL 307
              |: | :| | |:||
Db   296  LVKSEDCDLRLRTI 309

RESULT 15
Q66II1_XENTR
ID   Q66II1_XENTR PRELIMINARY;      PRT;    318 AA.
AC   Q66II1;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Pim3-prov protein.
GN   Name=pim3-prov;
OS   Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Silurana.
OX   NCBI_TaxID=8364;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Embryo;
RX   MEDLINE=22388557; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Embryo;
RA   Klein S., Gerhard D.S.;
RL   Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR   EMBL; BC081340; AAH81340.1; -; mRNA.
DR   SMR; Q66II1; 32-297.
DR   Ensembl; ENSXETG00000009354; Xenopus tropicalis.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
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Qy   176  DLNRGELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDM 235
              ||||||||||||||||||||||||||||||||||||||||||||||||  |||||||||||
Db   179  DLRSGELKLIDFGSGAVLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSATVWSLGVLLYDM 238

Qy   236  VCGDIPFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWM 290
              ||||||||  || ||||||| | |||| |  ||||||||| |||||| ||||||||
Db   239  VCGDIPFEQDEEILRGRLFPFRRRVSPECQQLIEWCLSLRPSERPSLDKL-CHPWM 292

RESULT 14
PIM3_XENLA
ID   PIM3_XENLA     STANDARD;     PRT;    323 AA.
AC   Q91822;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Serine/threonine-protein kinase Pim-3 (EC 2.7.1.37) (Pim-1).
GN   Name=PIM3; Synonyms=PIM1;
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   NUCLEOTIDE SEQUENCE, AND PHOSPHORYLATION SITES.
RX   MEDLINE=97256766; PubMed=9099695; DOI=10.1074/jbc.272.16.10514;
RA   Palaty C.K., Kalmar G., Tai G., Oh S., Amankawa L., Affolter M.,
RA   Aebersold R., Pelech S.L.;
RT   "Identification of the autophosphorylation sites of the Xenopus laevis
RT   Pim-1 proto-oncogene-encoded protein kinase.";
RL   J. Biol. Chem. 272:10514-10521(1997).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- PTM: Autophosphorylated.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC       subfamily.
CC   -!- CAUTION: Was originally (Ref.1) called Pim-1 but seems to
CC       represent the pim-3 isoform.
CC   ---------------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------------
DR   EMBL; L29495; AAA85389.1; -; mRNA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_Thr_pkin_AS.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Nucleotide-binding; Phosphorylation;
KW   Serine/threonine-protein kinase; Transferase.
FT   DOMAIN       40    291       Protein kinase.
FT   NP_BIND      46     54       ATP (By similarity).
FT   ACT_SITE    168    168       Proton acceptor (By similarity).
FT   BINDING      69     69       ATP (By similarity).
FT   MOD_RES       4      4       Phosphoserine (by autocatalysis)
FT                                (partial).
FT   MOD_RES     190    190       Phosphoserine (by autocatalysis).
FT   MOD_RES     205    205       Phosphothreonine (by autocatalysis)
FT                                (partial).
SQ   SEQUENCE   323 AA;  36964 MW;  AB4DD61E7A99A38F CRC64;

Query Match             66.2%;  Score 1105;  DB 1;  Length 323;
Best Local Similarity   65.3%;  Pred. No. 3e-73;
Matches  205;  Conservative   47;  Mismatches   50;  Indels   12;  Gaps   5;

Qy     1  MLLSKINSLAHLRAAPCN----DLHATKLAPGK-EKEPLESOYQVGPLLGSGGFGSVYS 54
              |||||: || :|  : |           |:|| |  ||  || :|| |||| | |||:|
Db     1  MLLSKFGSIAHI----CNPSNMEHLPVKILQPVKVDKEPFEKVYQVGSVVASGGFGTVYS 56
```

DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Cell division; Cell cycle; Kinase; Nucleotide-binding;
KW   Serine/threonine-protein kinase; Transferase.
SQ   SEQUENCE   318 AA; 36547 MW; 48CCF12797F01FDC CRC64;

Query Match   65.9%; Score 1101; DB 2; Length 318;
Best Local Similarity   70.3%; Pred. No. 5.9e-73;
Matches 204; Conservative 38; Mismatches 38; Indels 10; Gaps   4;

Qy   11 HLRAA-PCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSDNLPVAIKHV 69
         ||| | | : :|| ||| :||||||||||||:|:|||:|| |||||||||
Db   16 HLNSVFPKDDLPAV------KEPPENCYQVGPVIGTGGFGTVYSGVRISDKLPVAIKHV 68

Qy   70 EKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLILERPEPVQDL 129
         :|||| : ||| ||: :||||| :| || ||||||||||||: :|||||||||||||
Db   69 SRDRIGEMKHM-NGTLVPLEIYLLKKVSNGCRGVIRLLDWYERPDGFIIIMERPEPVQDL 127

Qy   130 FDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRGELKLIDFGS 189
         |||||||||| |||||:|| |::||||||| ||:|||||||||||:||:|:| :||||||
Db   128 FDFITERGALGEELATNFFRQVVEAVRHCHSCDVVHRDIKDENILIVDLRTAELKLIDFGS 187

Qy   190 GALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDIPFEHDEEI 249
         ||| :|||||||||||||||||||||:|| ||||:||||||||||||||||||||:||::
Db   188 GALLRDAVYTDFDGTRVYSPPEWIRFHKYHGRSATVWSLGILLYDMVCGDIPFEHDDEIL 247

Qy   250 RGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWM-QDVLLPQE 298
         ||||: :| :|:|||||||||||||| ||| |||::| |: : ::
Db   248 KGKIQYRCRVSRECQHLIEWCLSKRPSDRFSLEQILAHPWMSQDNFLDKK 297

Search completed: April 21, 2006, 12:58:33
Job time : 230 secs

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                 GenCore version 5.1.7
         Copyright (c) 1993 - 2006  Biocceleration Ltd.

OM protein - protein search, using sw model

Run on:    April 21, 2006, 12:54:54 ; Search time 40 Seconds
                              (without alignments)
                              752.896 Million cell updates/sec

Title:        US-10-664-421-1
Perfect score: 1670
Sequence:     1 MLLSKINSLAHLRAAPCNDL..........LLPQETAEIHLHSLSPGPSK 313

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched:      283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:      283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :  PIR_80:*
            1: pir1:*
            2: pir2:*
            3: pir3:*
            4: pir4:*

Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1670	100.0	313	1	TVHUP1	protein kinase (EC
2	1636	98.0	313	1	S26298	protein kinase (EC
3	1582	94.7	313	1	TVMSP1	protein kinase (EC
4	881.5	52.8	370	1	S55333	protein kinase pim
5	617	36.9	363	2	T22255	hypothetical prote
6	486	29.1	409	2	T15435	hypothetical prote
7	386	23.1	481	2	I49072	protein kinase - m
8	380	22.8	1398	2	T13741	hypothetical prote
9	376	22.5	1101	2	S66730	hypothetical prote
10	367	22.0	1358	2	S33653	probable serine/th
11	366	21.9	504	2	T10449	probable serine/th
12	361	21.6	651	2	S52244	p69Bg3 protein - A
13	361	21.6	798	2	JC7500	qik protein - chic
14	360	21.6	512	1	JC1446	serine/threonine-s
15	359	21.4	511	1	A56009	serine/threonine-s
16	357	21.4	512	2	T52633	serine/threonine-s
17	352	21.1	512	2	T07788	probable serine/th
18	348	20.8	472	2	B90100	SNF-related kinase
19	347.5	20.8	469	2	B84644	probable protein k
20	347.5	20.8	887	2	T20941	hypothetical prote
21	345	20.7	726	2	T33998	probable serine/th
22	342.5	20.5	489	2	T04862	probable serine/th
23	342.5	20.5	1558	2	T29253	hypothetical prote
24	341.5	20.4	414	2	JN0323	Ca2+/calmodulin-de
25	341	20.4	513	1	S60304	serine/threonine-s
26	339.5	20.3	504	2	T07415	probable serine/th
27	337	20.2	502	2	T02306	probable protein k
28	337	20.2	713	2	S27966	probable serine/th
29	336.5	20.1	445	2	T50802	serine/threonine p
30	335	20.1	745	2	G01025	serine/threonine p
31	333.5	20.0	1518	2	S37928	probable purine nu
32	331.5	19.9	774	2	I48609	probable serine/th
33	331	19.8	435	2	B84707	probable protein k
34	330.5	19.8	339	2	S56719	serine/threonine-s
35	330.5	19.8	520	2	G86414	probable protein k
36	330.5	19.8	553	1	T02139	calcium-dependent
37	328	19.6	591	2	S54788	calcium-stimulated
38	327	19.6	582	2	B84721	probable calcium-d
39	326.5	19.6	746	2	S62365	SNF1-related prote
40	325.5	19.5	442	2	T48203	hypothetical prote
41	325	19.5	1246	2	G89287	protein H39B23.1 [
42	324.5	19.4	713	2	T37886	probable serine/th
43	324	19.4	401	2	B90120	SNF1-related prote
44	323	19.3	461	2	T14822	probable serine/th
45	323	19.3	473	1	S59941	serine/threonine-s

ALIGNMENTS

```
RESULT 1
TVHUP1
protein kinase (EC 2.7.1.37) pim-1 - human
N;Alternate names: kinase-related transforming protein pim-1; pim-1 proto-oncogene prot
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1989 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C;Accession: JU0327; A46554; A27476; I58412
R;Reeves, R.; Spies, G.A.; Kiefer, M.; Barr, P.J.; Power, M.
Gene 90, 303-307, 1990
A;Title: Primary structure of the putative human oncogene, pim-1.
A;Reference number: JU0327; MUID:90382681; PMID:2205533
A;Accession: JU0327
A;Molecule type: DNA
A;Residues: 1-313 <REE>
A;Cross-references: UNIPROT:P11309; UNIPARC:UPI000001060; GB:M27903; NID:g189958; PIDN
R;Meeker, T.C.; Nagarajan, L.; ar-Rushdi, A.; Croce, C.M.
J. Cell. Biochem. 35, 105-112, 1987
A;Title: Cloning and characterization of the human PIM-1 gene: a putative oncogene rela.
A;Reference number: A46554; MUID:88115604; PMID:3429489
A;Accession: A46554
A;Molecule type: mRNA
A;Residues: 1-313 <MEE>
A;Cross-references: UNIPARC:UPI000001060; GB:M24779; NID:g1066790; PIDN:AAA81553.1; PI
R;Zakut-Houri, R.; Hazum, S.; Givol, D.; Teleman, A.
Gene 54, 105-111, 1987
A;Title: The cDNA sequence and gene analysis of the human pim oncogene.
A;Reference number: A27476; MUID:87277423; PMID:3475233
A;Accession: A27476
A;Molecule type: mRNA
A;Residues: 1-14, 'RA',17-313 <ZAK>
A;Cross-references: UNIPARC:UPI00001987C; GB:M16750; NID:g189956; PIDN:AAA60089.1; PID
R;Domen, J.; Von Lindern, M.; Hermans, A.; Breuer, M.; Grosveld, G.; Berns, A.A.
Oncogene Res. 1, 103-112, 1987
A;Title: Comparison of the human and mouse PIM-1 cDNAs: Nucleotide sequence and immunol.
A;Reference number: I58412; MUID:88217305; PMID:3329709
A;Accession: I58412
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-313 <DOM>
A;Cross-references: UNIPARC:UPI000001060; GB:M54915; NID:g189961; PIDN:AAA36447.1; PID
C;Comment: Pim-1 autophosphorylates at unknown sites.
C;Genetics:
C;Gene: GDB:PIM1
A;Cross-references: GDB:119495; OMIM:164960
A;Map position: 6p21.2-6p21.2
A;Introns: 28/2; 63/3; 80/3; 203/1; 262/1
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threoni.
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogen
F;36-290/Domain: protein kinase homology <KIN>
F;44-52/Region: protein kinase ATP-binding motif
```

```
F;67/Active site: Lys #status predicted

Query Match            100.0%;   Score 1670;  DB 1;   Length 313;
Best Local Similarity  100.0%;   Pred. No. 1.9e-76;
Matches  313;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy  241 PFEHDEEIIRGQVYFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 PFEHDEEIIRGQVYFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy  301 EIHLHSLSPGPSK 313
          |||||||||||||
Db  301 EIHLHSLSPGPSK 313
```

RESULT 2
S26298
protein kinase (EC 2.7.1.37) pim-1 - rat
N;Alternate names: kinase-related transforming protein pim-1; pim-1 proto-oncogene prote
C;Species: Rattus norvegicus (Norway rat)
A;Experimental source: testis
C;Date: 25-Feb-1994 #sequence_revision 21-Jan-1997 #text_change 09-Jul-2004
C;Note: testis-specific transcript is shorter and more stable than the somatic transcrip
C;Comment: Pim-1 autophosphorylates at unknown sites.
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
A;Note: in testis may be involved in signal transduction events of normal germ cell matu
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene
F;36-290/Domain: protein kinase homology <KIN>
F;44-52/Region: protein kinase ATP-binding motif
F;67/Active site: Lys #status predicted
A;Cross-references: UNIPROT:P26794; UNIPARC:UPI0000131AD6; EMBL:X63675; NID:g56902; PID...
A;Residues: 1-313 <WIN>
A;Molecule type: mRNA
A;Reference number: S26298; MUID:92319652; PMID:1620615
A;Title: Characterization of the testes-specific pim-1 transcript in rat.
R;Winget, D.; Reeves, R.; Magnuson, N.S.
Nucleic Acids Res. 20, 3183-3189, 1992
A;Accession: S26298
A;Genetics:
A;Gene: pim-1

```
Query Match             98.0%;   Score 1636;  DB 1;   Length 313;
Best Local Similarity   97.1%;   Pred. No. 9.2e-75;
Matches  304;  Conservative  6;  Mismatches  3;  Indels  0;  Gaps  0;

Qy    1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
          |||||||||||||||:|||||||||||||||||||||||||||||||||||||||||||
Db    1 MLLSKINSLAHLRARPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy  241 PFEHDEEIIRGQVYFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
          ||||||||:|||::||||:||||||||:|||:|||||||:|||||||||::|||||:|||
Db  241 PFEHDEEIVKGQVFFRQRVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLLPQAAS 300

Qy  301 EIHLHSLSPGPSK 313
          ||||||||||:||
Db  301 EIHLHSLSPGSSK 313
```

RESULT 3
TVMSP1
protein kinase (EC 2.7.1.37) pim-1 - mouse
N;Alternate names: kinase-related transforming protein pim-1; pim-1 proto-oncogene prote
C;Species: Mus musculus (house mouse)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
C;Accession: A24169
R;Selten, G.; Cuypers, H.T.; Boelens, W.; Robanus-Maandag, E.; Verbeek, J.; Domen, J.; ...
Cell 46, 603-611, 1986
A;Reference number: A24169; MUID:8272109; PMID:3015420
A;Title: The primary structure of the putative oncogene pim-1 shows extensive homology w...
A;Accession: A24169
A;Molecule type: DNA
A;Residues: 1-313 <SEL>
A;Cross-references: UNIPROT:P06803; UNIPARC:UPI00000294AF; GB:M13945; GB:M13946; NID:g2...
C;Comment: Pim-1 autophosphorylates at unknown sites.
C;Genetics:
A;Gene: pim-1
A;Introns: 28/1; 63/3; 80/3; 203/1; 262/1
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
C;Superfamily: kinase-related transforming protein; protein kinase homology <KIN>
C;Keywords: ATP; autophosphorylation; phosphotransferase; proto-oncogene; serine/threoni
F;36-290/Domain: protein kinase homology <KIN>
F;44-52/Region: protein kinase ATP-binding motif
F;67/Active site: Lys #status predicted

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Query Match             94.7%;   Score 1582;  DB 1;   Length 313;
Best Local Similarity   93.9%;   Pred. No. 4.4e-72;
Matches  294;  Conservative 10;  Mismatches  9;  Indels  0;  Gaps  0;

Qy    1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
          |||||||||||||:||||||||||||||||||||||||||||||||||||||||||||:
Db    1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
          ||||||||||||||||||||:|||:||||||||||||||||||||||||||||||||:||
Db  121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180

Qy  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy  241 PFEHDEEIIRGQVYFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
          ||||||||::|||:||||:|||||||:|||:|||||||:|||||:||||||::|||||||
Db  241 PFEHDEEIVKGQVFFRQRVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLLPQAAS 300

Qy  301 EIHLHSLSPGPSK 313
          ||||||||||:||
Db  301 EIHLHSLSPGSSK 313
```

RESULT 4
S55333
protein kinase pim-2 (EC 2.7.1.-) - mouse

```
C;Species: Mus musculus (house mouse)
C;Date: 10-Oct-1995 #sequence revision 21-Jan-1997 #text_change 09-Jul-2004
C;Accession: S55333; A43093; B43093
R;van der Lugt, N.M.T.; Domen, J.; Verhoeven, E.; Linders, K.; van der Gulden, H.; Allen
EMBO J. 14, 2536-2544, 1995
A;Title: Proviral tagging in B-mu-myc transgenic mice lacking the Pim-1 proto-oncogene 1
A;Reference number: S55333; MUID:95300786; PMID:7781606
A;Accession: S55333
A;Molecule type: mRNA
A;Residues: 1-370 <VAN>
A;Cross-references: UNIPROT:Q62070; UNIPARC:UPI0000028629; GB:L41495; NID:g765065; PIDN:
A;Note: 40K form
A;Accession: A43093
A;Molecule type: mRNA
A;Residues: 'M',27-370 <VA2>
A;Cross-references: UNIPARC:UPI000000278BB; GB:L41495; NID:g765065; PIDN:AAA98923.1; PID:
A;Note: 37K form
A;Accession: B43093
A;Molecule type: mRNA
A;Residues: 'M',61-370 <VA3>
A;Cross-references: UNIPARC:UPI000000278BF; GB:L41495; NID:g765065; PIDN:AAA98924.1; PID:
A;Note: 34K form
C;Comment: Pim-2 autophosphorylates at unknown sites.
C;Genetics:
A;Gene: Pim-2
A;Map position: X
A;Start codon: CTG
A;Note: locus between A-raf and Act-7, near Kv4.1
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: alternative initiators; ATP; autophosphorylation; phosphoprotein; phosphotra
F;89-345/Domain: protein kinase homology <KIN>
F;97-105/Region: protein kinase ATP-binding motif
F;120/Active site: Lys #status predicted

Query Match     52.8%;  Score 881.5;  DB 1;  Length 370;
Best Local Similarity   56.6%;  Pred. No. 2.7e-37;
Matches 171;  Conservative   41;  Mismatches 85;  Indels    5;  Gaps     2;

Qy    12 LRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSDNLPVAIKHVEK 71
            :|| :|: :|:: |::||||||||||||||  |||||| ||||:||
Db    65 LQGHSPPVTPTQPPGGKDRAAFRAEYRLGPLLGKGGFGTVFAGHRVTDRRQVAIKVISR 124

Qy    72 DRISDWGELPNGTRVPMEVVLLKKV--SSGFSGVIRLLDWFERPDSFVLILERPEPVQDL 129
            :|: ||||||||||||||||| ||: :||:|||||||||||: |||| ||||||||||
Db   125 NRVLGWSTVSDSVTCPLEVALLWKVGEGNGHPGVIRLLDWFETPEGFMLVLERRMPAQDL 184

Qy   130 FDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRGELKLIDFGS 189
            |||||||||||||||||||||| |:|||:||||||||||||||||| |||| ||||||
Db   185 FDYITEKGPLGESCSRSFFTQVVAAVQHCHARGVIRLLDWSSPPEWISRHQVHALPATVW 244

Qy   190 GALLKDTVTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDIPFEHDEII 249
            |||| |||||||||||||||||||  ||:|||||||||||||||||||||||| ||
Db   245 GALLHDEPYTDFDGTRVYSPPEWISRHQVHALPATVWSLGVLLYDMVCGDIPFERDQEIL 304

Qy   250 RGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETAEIHLHSLSP 309
            |||||||||||||||||||| :|| :||| |||| | |||:
Db   305 EAELHFPAHVSPDCCALIRRCLAPKPCSRPSLEETILLDPWMQS---PAEEKPINSSKGSP 361

Qy   310 GP 311
            |
Db   362 TP 363


RESULT 5
T22255
hypothetical protein F45H7.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Dec-2004
C;Accession: T22255
R;Percy, C.
submitted to the EMBL Data Library, June 1994
```

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A;Reference number: Z19538
A;Accession: T22255
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-363 <WIL>
A;Cross-references: UNIPROT:Q20443; UNIPARC:UPI0000001755A4; EMBL:Z34800; PIDN:CAA84323.1
A;Experimental source: clone F45H7
C;Genetics:
A;Gene: CESP:F45H7.4
A;Map position: 3
A;Introns: 72/3; 160/3; 310/1
C;Superfamily: protein kinase homology

Query Match     36.9%;  Score 617;  DB 2;  Length 363;
Best Local Similarity   45.3%;  Pred. No. 3.5e-24;
Matches 120;  Conservative   49;  Mismatches   90;  Indels    6;  Gaps     3;

Qy    35 ESQYQVGPLLGSGGFGSVYSGIRVSDNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLK 94
            |:|| ||| |||||||||||||||||||||  :| : : :|||| ::|| ::|
Db    28 KKNYKLKAELGRGGFGVVYRAVRTCDNALAVKFIERSNVKEWARI-NGEQVPMEICMLA 86

Qy    95 KVSSGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELARSFFWQVLEA 154
            |  |:|||||||||||| :|||||| | :|| :||||||||||||| |||||||||
Db    87 KCSK-VRGVIRLLDWYSIPEGFLIVMERPYPCIDMFDFIKGQKISEDMARFLFRQIAVT 145

Qy   155 VRHCHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVTDFDGTRVYSPPEWIR 214
            |  |:| |||||||||:||||:|||| :|:|||||| |:||||| |:|||||||||||
Db   146 VHECVQNRVLHRDLKDENIVIDLVTGSTKLIDFGAATVLRRSQYSDFQGTRLYCPPEWFL 205

Qy   215 YHRYHGRSAAVWSLGILLYDMVCGDIPFEHDEI----IRGQVFFRQRVSSECQHLIRWC 270
            |  || || |||||||:||||||||||||  |:     :|: |||| |||||||||||
Db   206 HSLYLGREAAVWSLGVLLYNSLNGRLPFRNEKDICTAHLLGPLPFFVPVSAEVKDLISKC 265

Qy   271 LALRPSDRPTFEEIQNHPWMQDVLL 295
            |||||||||||||| |||||||||
Db   266 LTFDPFPQRCSLEAILNHPWVKQQTL 290


RESULT 6
T15435
hypothetical protein C06E8.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T15435
R;Favello, A.
A;Description: The sequence of C. elegans cosmid C06E8.
submitted to the EMBL Data Library, February 1994
A;Reference number: Z18350
A;Accession: T15435
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-409 <FAV>
A;Cross-references: UNIPARC:UPI000017B744; EMBL:U00034; NID:g458983; PID:g458986; PIDN..
A;Experimental source: strain Bristol N2
C;Genetics:
A;Gene: CESP:C06E8.3
A;Introns: 24/1; 76/3; 107/2; 145/3; 199/1; 307/1; 375/1

Query Match     29.1%;  Score 486;  DB 2;  Length 409;
Best Local Similarity   35.8%;  Pred. No. 1.2e-17;
Matches 105;  Conservative   55;  Mismatches   55;  Indels  125;  Indels    8;  Gaps     5;

Qy     1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSG-IRVS 59
            |:|| ::| :  :|||| : |::: :  ::|  :||| :|||| ||||| || |||
Db     1 MIKRKLQDLAVCCSYQVDFLHEKK---HSVKSFKRKYEVLDEIGRGGFGVIVYEATTRQD 56

Qy    60 DNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVVSSGGFGSVIRLLDWFERPDSFVLI 119
            ||||||||| ||: : :|: |:| ::|  ||:|  : ::| ||:||||||||||| ||
Db    57 GQQPVAVKFVQHKHVRSW-TMTCRQLIPSEVCHL-ETCEDIPGVIKILDWFANSKGFLIV 114

Qy   120 LERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHN-CGVLHRDIKDENILIDLN 178
            ||||| :|| |||| | :|| :| |:||||||| ||:|||| |||||||||||:|| |:|
Db   115 MERPANCMDLFDMSVHGPLNEDMGKFIFKQVITTVFNMYSKGLLHRDIKDENLIVNMN 174
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Qy      179  RGELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYRYHGRSAAVWSLGILLYDMVCG 238
                  ||:|||:|||  | ||||| |||||||||:||:::||||||::::|
Db      175  TGEVKLVDFGATAYAEKATKKEFQGTRSYCPPEWFRDQLYLPLEATSWSLGVLLFILLTG 234

Qy      239  DIPPEHDEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQ 291
                  |||||||| :||||||||||||||||||||||||||||||||||
Db      235  KLPFRNEIQICLGNVKFPPDLSKEVCQLVKSCLTTSTSARASLAQIAAHPWME 287


RESULT 7
I49072
protein kinase - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Oct-2004
C;Accession: I49072
R;Ruiz, J.C.; Conlon, F.L.; Robertson, E.J.
A;Title: Identification of novel protein kinases expressed in the myocardium of the deve
Mech. Dev. 48, 153-164, 1994
A;Reference number: 149071; MUID:95200798; PMID:7893599
A;Accession: I49072
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-481 <RES>
A;Cross-references: UNIPARC:UPI000017A422; EMBL:U11494; NID:g595420; PIDN:AAA67926.1; PI
C;Keywords: ATP
F;71-324/Domain: protein kinase homology <KIN>
F;79-87/Region: protein kinase ATP-binding motif

Query Match           23.1%;  Score 386;  DB 2;  Length 481;
Best Local Similarity 33.9%;  Pred. No. 1.3e-12;
Matches    99;  Conservative 53;  Mismatches 120;  Indels 20;  Gaps 10;

Qy       18  NDLHATKLAPGKEKEPLE-SQYQVGPLLGSGGFGSV-YSGIRVSDNLPVAIKHVEKDRIS 75
                 :: :::||  |  ||| ||:|||||||||||| ||||:|||   ||:||||:|
Db       52  SEFRAVPSGTGRSQKPLRVGFYDVERTLGKGNFAVVKLRGHRVT-KTQVAIKIIDKTRL- 109

Qy       76  DWGELPNGTRVPMEVVLKKVSSGFSGVIRLLDWFERPDSFVLILERPEVQDLFDFITE 135
                 || |||||| |||| |  : |||  |:| |:|||||||||||:||:|||||||||
Db      110  ---DSSNLEKIYREVQLMKLLN--HPNIKLYQVMETKDMLYIVTEFAKN-GEMFDYLTS 163

Qy      136  RGALQEELARSFFWQVLEAVRHCHCNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLK- 194
                 ||| ||||| ||::|||||||||:|:||||||||||:| ::|||||||||||||||||
Db      164  NGHLSENEARQKFWQILSAVEYCHNHHIVHRDLKTENLLLDSNM-DIKLADFGFGNFYKP 222

Qy      195  DTVYTDFDGTRVYSPPEWIRYRYHGRSAAVWSLGILLYDMVCGDIPPEHD-----EEI 248
                 ||| || ||||||:||||||||:|||||||||||||||||||||||||:|     :|
Db      223  GEPLSTCVGSPPYAAPEVFEGKEYEGPQLDVWSLGVVLVLVCGSSLPFDGPNLPTLRQRV 282

Qy      249  IRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQ--DVLLPQE 298
                 ||||||||||||||||||||||||||||||||||||||||||  :|||:|
Db      283  LEGRFRIPFFMSQDCETLIRRMLVVDPAKRITIAQIRQHRWMQADPTLLQQD 334


RESULT 8
T13741
hypothetical protein 22E5.8 - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C;Accession: T13741
R;Murphy, L.; Harris, D.; Barrell, B.
submitted to the EMBL Data Library, April 1999
A;Description: Sequencing the distal X chromosome of Drosophila melanogaster.
A;Reference number: Z17668
A;Accession: T13741
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1398 <MUR>
C;Genetics:
A;Cross-references: UNIPROT:O77268; UNIPARC:UPI0000820A3; EMBL:AL031765; NID:e1371523;
A;Introns: 205/3; 227/1; 322/3; 688/3; 782/3; 814/2; 1363/3
A;Note: EG:22E5.8
```

```
Query Match           22.8%;  Score 380;  DB 2;  Length 1398;
Best Local Similarity 33.3%;  Pred. No. 6.2e-12;
Matches    92;  Conservative 57;  Mismatches 109;  Indels 18;  Gaps 9;

Qy       29  KEKEPLE-SQYQVGPLLGSGGFGSV-YSGIRVSDNLPVAIKHVEKDRISDWGELPNGTRV 86
                 |||||| ||:|||||||||||| ||||:||||||||||||||||||::|||||||||
Db      131  KLKEPMRVGFYDIERTIGKGNFAVVKLARHRITKN-EVAIKIIDKSQL----DQTNLQKV 185

Qy       87  PMEVVLKKVSSGFSGVIRLLDWFERPDSFVLILERPEVQDLFDFITERGALQEELARS 146
                 :::| :||::  : :||| ||:|:||||:||:||||||::::||:||||:|||||||
Db      186  YREVEIMKRLK--HPHIIKLYQVMETKNMIYIVSEYASQ-GEIFDYIAKYGRMSESAARF 242

Qy      147  FFWQVLEAVRHCHCNCGVLHRDIKDENILIDLNRGELKLIDFG-SGALLKDTVYTDFDGTR 205
                 ||||||||||||||:|||||||||||||:|||||||||||||| :||||||||:||||||
Db      243  KFWQIISAVEYCHKKGIVHRDLKAENLLLDNM-NKIADFGFSNHFKPGELLATWCGSP 301

Qy      206  VYSPPEWIRYRYHGRSAAVWSLGILLYDMVCGDIPPEHD------EEIIRGQVFFRQRV 259
                 |||||||||||||||||||||||||||||||||||:|||      |||||||||||||
Db      302  PYAAPEVFEGKQYTGPEIDIWSLGVVLYLVCGALPFDGSTLQSLRDRVLSGRFRIPFFM 361

Qy      260  SSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLL 295
                 ||||||||||||||||||||||||||||||||:|||
Db      362  SSECEHLIRRMLVLEPTRRYTIDQIKRHRWMCPELL 397


RESULT 9
S66730
hypothetical protein YOL045w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein O2034
C;Species: Saccharomyces cerevisiae
C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 05-Oct-2004
C;Accession: S66730
R;Ansorge, W.; Benes, V.; Rechmann, S.; Schwager, C.; Teodoru, C.; Voss, H.; Wiemann, S.
submitted to the Protein Sequence Database, July 1996
A;Reference number: S66723
A;Accession: S66730
A;Molecule type: DNA
A;Residues: 1-1101 <ANS>
A;Cross-references: UNIPROT:Q08217; UNIPARC:UPI000012DF35; EMBL:Z74788; NID:g1419846; PI
A;Experimental source: strain S288C
C;Genetics:
A;Cross-references: SGD:S0005405
A;Map position: 15L
C;Keywords: ATP
F;833-1099/Domain: protein kinase homology <KIN>
F;847-855/Region: protein kinase ATP-binding motif

Query Match           22.5%;  Score 376;  DB 2;  Length 1101;
Best Local Similarity 32.6%;  Pred. No. 8e-12;
Matches    87;  Conservative 59;  Mismatches 105;  Indels 16;  Gaps 6;

Qy       36  SQYQVGPLLGSGGFGSVYSGIRVSDNLPVAIKHVEKDRI--SDWGELPNGTRVPMEVVLL 93
                 ||:|||||||||||||||||||||||||||||||||||  ||:|||||||||||:|||
Db      839  SDFTILQVMGEGAYGKVNLCIHNREHYIVVKMIFKERILVDTWVRDRKLGTIPSEQIM 898

Qy       94  KKVS-SGFSGVIRLLDWFERPDSFVLILERPEVQ-----DLFDFITERGALQEELARS 146
                 |||  ||:||||||||||||||:|||||||||||     |||||||||||:||||||
Db      899  ATLNKNSQENLKLLDFFEDDDYYI----ETPVHGETGSIDLFDVIEFKKDMVEHEAKL 954

Qy      147  FFWQVLEAVRHCHCNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVVTDFDGTRV 206
                 ||||||||||||||:|||||||||||||:|||||||||||||:|||||||||:||||||
Db      955  VFKQVVASIKHLHDQGIVHRDIKDENVIVD-SHGFVKLIDFGSAAYIKSGPFDVFVGTMD 1013

Qy      207  YSPPEWIRYRYHGRSAAVWSLGILLYDMVCGDIPFEHDEEIIRGQVFF--RQRVSSECQ 264
                 ||||||||||||||||||||||||||||||||||||:|||||||||||  |||||||||
Db     1014  YAAPEVLGGSSYKGKPQDIWALGVLLYTIIYKENPYNIDEILEGELRFDKSEHVSSECI 1073

Qy      265  HLIRWCLALRPSDRPTFEEIQNHPWMQ 291
                 ||:| ||||||||||||||:||||||
Db     1074  SLIKRILTRBVDKRPTIDEIYEDKWLK 1100
```

RESULT 10
S33653
probable serine/threonine protein kinase (EC 2.7.1.-) - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein YAL002; protein YAL017w; secretory protein SSP138
C;Species: Saccharomyces cerevisiae
C;Date: 30-Sep-1993 #sequence_revision 02-Aug-1994 #text_change 05-Oct-2004
C;Accession: S33653; S33717; S36732; JH0486
R;Clark, M.W.; Zhong, W.W.; Keng, T.; Storms, R.K.; Ouellette, B.F.F.; Barton, A.; Kabac
Yeast 9, 543-549, 1993
A;Title: The YAL017 gene on the left arm of chromosome I of Saccharomyces cerevisiae enc
A;Reference number: S33653; MUID:9311122; PMID:8322517
A;Accession: S33653
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-1358 <CLA>
A;Cross-references: UNIPROT:P31374; UNIPARC:UPI000017A449; EMBL:L05146
R;Ouellette, F.; Clark, M.W.; Keng, T.; Storms, W.; Zeng, B.; Fortin, N.; D
submitted to the EMBL Data Library, January 1993
A;Description: Sequencing of Chromosome I from Saccharomyces cerevisiae: analysis of a 3
A;Reference number: S36711
A;Accession: S36717
A;Molecule type: DNA
A;Residues: 1-864,867-1358 <OUE>
A;Cross-references: UNIPARC:UPI00000052EA6; EMBL:L05146; NID:g171851; PIDN:AAC04940.1; PI
R;Clark, M.W.; Zhong, W.W.; Keng, T.; Storms, R.K.; Barton, A.; Kaback, D.B.; Bussey, H.
Yeast 8, 133-145, 1992
A;Title: Identification of a Saccharomyces cerevisiae homolog of the SNF2 transcriptiona
A;Reference number: S22266; MUID:92221690; PMID:1561836
A;Accession: S36732
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-862 <CL2>
A;Cross-references: UNIPARC:UPI000017A44A; EMBL:S93805
R;Sidhu, R.S.; Mathewes, S.; Bollon, A.P.
Gene 107, 111-118, 1991
A;Title: Selection of secretory protein-encoding genes by fusion with PHO5 in Saccharomy
A;Reference number: JH0483; MUID:92077420; PMID:1743509
A;Accession: JH0486
A;Molecule type: DNA
A;Residues: 1-72,'E','74-154 <SID>
A;Cross-references: UNIPARC:UPI000017A44B
C;Genetics:
A;Gene: SGD:FUN31; SSP138
A;Cross-references: SGD:S0000015; MIPS:YAL017w
A;Map position: 1L
F;Keywords: ATP; glycoprotein; phosphotransferase; serine/threonine-specific protein kin
F;1096-1356/Domain: protein kinase homology <KIN>
F;1104-1112/Region: protein kinase ATP-binding motif
F;8,128/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;1232/Active site: Asp #status predicted

Query Match   22.0%; Score 367; DB 2; Length 1358;
Best Local Similarity   33.7%; Pred. No. 2.7e-11;
Matches   87; Conservative 53; Mismatches 102; Indels 16; Gaps   6;

Qy   44 LGSGGFGSVYSGIRVSDNLPVAIKHVEKDRI--SDWGELPNGTRVPMEVVLLKKVS-SGF 100
              ::| ||:||| |::| | | ::||| |||:|
Db   1104 MGEGAYGKVNLCIHKKNRYIVIKMIFKERILVDTWVRDRKLGTIPSEIQIMATLNKKPH 1163

Qy   101 SGVIRLLDWFERPDSFVLILERPEPVQ-------DLFDITERGALQEELARSFFWQVLEA 154
             :||||||| | : : |||:| ||| | ::::
Db   1164 ENILRLLDFFEDDYYI---ETPVHGETGCIDLFDLIEFKINMTBFEAKLIFKQVVAG 1219

Qy   155 VRHCHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIR 214
              || || : :| |: |||: :| ::| ||||||
Db   1220 IKHLHDQGIVHRDIKDENVIVD-SKGFVKIIDFGSGAAYVKSGPFFVFVGTIDYAAPEVLG 1278

Qy   215 YHRYHGRSAAVWSLGILLYDMVCGDIPFEHDEEIIRGQVFPR--QRVSSECQHLIRWCLA 272
             |||||||||||:|||:|| || |||||||: || | |:| ||:| |:| ||:|
Db   1279 GNPYEGQPQDIWAIGILLYTVVFFKENPFYNIDEILEGDLKFNNAEBVSEDCIELIKSILN 1338

Qy   273 LRPSDRPTFEEIQNHPWM 290
             ||| ||| :| ||| |

Db   1339 RCVPKRPTIDDINNDKWL 1356

RESULT 11
T10449
probable serine/threonine-specific protein kinase (EC 2.7.1.-) - cucumber
N;Alternate names: SNF1-related protein kinase
C;Species: Cucumis sativus (cucumber)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 05-Oct-2004
C;Accession: T10449
R;Gumpel, N.J.
submitted to the EMBL Data Library, December 1996
A;Reference number: Z17020
A;Accession: T10449
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-504 <GUM>
A;Cross-references: UNIPROT:P93113; UNIPARC:UPI0000A04B92; EMBL:Y10036
A;Experimental source: cv. Masterpiece; cotyledon
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threoni
C;Superfamily: SNF1-related protein kinase; protein kinase homology
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F;6-260/Domain: protein kinase homology <KIN>

Query Match   21.9%; Score 366; DB 2; Length 504;
Best Local Similarity   34.4%; Pred. No. 1.3e-11;
Matches   90; Conservative 51; Mismatches 105; Indels 16; Gaps   8;

Qy   38 YQVGFPLLGSGGFGSVYSGIRVSDNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVS 97
             ::: || ||| |||||| :|:| | | ::||| |||:|
Db   8 YKLGKTLGIGSFGKVKIAEHALTGHKVAIKILNRRKIKN--LDMEEKVRREIKILRLFM 64

Qy   98 SGFSGGVIRLLDWFERPDSFVLILERPEPVQDLFDPITERGALQEELARSFFWQVLEAVRH 157
                || | :|||||| | || :|: |||:| ||| | ::
Db   65 --HPHIIRLYEVIETPSDIYVMEYVKS-GELFDYIVEKGRLQEDEARNFFQQIISGVEY 121

Qy   158 CHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVYTDFD-GTRVYSPPEWIRYH 216
             | | |:||: |:| ||: || :::| | |:
Db   122 CHRNMVVHRDLKPENLLLD-SKCNVKIADFGLSNIMRDGHFLKTSCGSPNYAAPEVISGK 180

Qy   217 RYHGRSAAVWSLGILLYDMVCGDIPPEHDEI------IRGQVF-FRQRVSSECQHLIRW 269
              | |||||:||||:|| :| | | :| : | | |
Db   181 LYAGPEVDVWSCGVILYALLCGTLPFD-DENIPNLFKKIKGGIYTLPSHLSSGARELIPS 239

Qy   270 CLALRPSDRPTFEEIQNHPWMQ 291
             | ||| ||| :| ||| | |
Db   240 MLVVDDMKRITIPEIRQHPWFQ 261

RESULT 12
S52244
p69Eg3 protein - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 07-May-1995 #sequence_revision 03-Aug-1995 #text_change 05-Oct-2004
C;Accession: S52244
R;Roghi, C.; le Guellec, R.; Paris, J.; Couturier, A.; Philippe, M.
submitted to the EMBL Data Library, October 1992
A;Description: Eg3, selected by differential screening encodes a new Xenopus protein kin
A;Reference number: S52243
A;Accession: S52244
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-651 <ROG>
A;Cross-references: UNIPROT:Q91821; UNIPARC:UPI000017A463; EMBL:Z17205; NID:g609283; PII
C;Keyword: ATP
F;11-265/Domain: protein kinase homology <KIN>
F;19-27/Region: protein kinase ATP-binding motif

Query Match   21.6%; Score 361; DB 2; Length 651;
Best Local Similarity   34.8%; Pred. No. 2.8e-11;
Matches   94; Conservative 51; Mismatches 103; Indels 22; Gaps   8;

Qy   32 EPLESQYQVGPLLGSGGFGSVYSGIRVSDNLPVAIKHVEKDRISDWGELPNGTRVPMEVV 91
          ||| :|||||||| ||
Db   7 EELLKYYELHETVGTGGFAKVKLASHLITGEKVAIKIMDKESLGD--DLP---RVKTEID 61

Qy   92 LLKKVSSGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELARSFFWQV 151
          :|||| |||||||:| |||
Db   62 AMKNLS--HQHVCRLYHVIETPKKIFMVLEYC-PGGELFDYIIAKDRLTEEEARVFFRQI 118

Qy   152 LEAVRHCHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVYTFD-----GTRV 206
          |||| |||||||||||| || ||||||||||||||:||||||||
Db   119 VSAVAYIHSQGYAHRDLKPENLLIDEDQ-NLKLIDFGLCAKPKGGL--DYHLMTCCGSPA 175

Qy   207 YSSPEWIRYHRYHGRSAAVWSLGILLYDMVCGDIPFEHD------EEIIRGQVFFRQRVS 260
          | |:| | | ::|||||||||||||:||||||: |:| :||
Db   176 YAAPELIIQGKAYIGSEADIWSMGVLMYALMCGYLPFDDDNVMVLYKKIMRGKYIEIPKWLS 235

Qy   261 SECQHLIRWCLALRPSDRPTFEEIQNHPWM 290
          |: ||||||||||||||||:|||||
Db   236 PGSVLLLSQMMQVDPKKRITVKGHLLNHPWL 265

RESULT 13
JC7500
qik protein - chicken
N;Alternate names: Qin-induced kinase
C;Species: Gallus gallus (chicken)
C;Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 09-Jul-2004
C;Accession: JC7500
R;Xia, Y.; Zhang, Z.; Kruse, U.; Vogt, P.K.; Li, J.
Biochem. Biophys. Res. Commun. 276, 564-570, 2000
A;Title: The new serine-threonine kinase, Qik, is a target of the qin oncogene.
A;Reference number: JC7500
A;Contents: Embryo fibroblasts
A;Accession: JC7500
A;Molecule type: mRNA
A;Residues: 1-798 <XIA>
A;Cross-references: UNIPROT:Q91A88; UNIPARC:UPI000044792; GB:AF219232
C;Comment: This protein, a member of the AMPK/SNF1 family of serine/threonine kinases, f
C;Genetics:
A;Gene: qik
C;Keywords: protein kinase

Query Match   21.6%;   Score 361; DB 2; Length 798;
Best Local Similarity 32.7%;   Pred. No. 3.4e-11;
Matches 88;   Conservative 50;   Mismatches 115;   Indels 16;   Gaps   7;

Qy   38 YQVGPLLGSGGFGSVYSGIRVSDNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVS 97
          ||||||||||||||||||||||||||||||||||||||||||||||||||| ::
Db   26 YDIERTLGKGNFAVVKLARHRVKTQVAIKIIDKTRL----DPSNLEKIYREVQIMKLLN 81

Qy   98 SGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRH 157
          ||||||||||||||||||||| : :||
Db   82 --HPHIIKLYQVMETKDMLYIVTEFAKN-GEMFDHLTSNGHLSESEARKKFWQILSAVEY 138

Qy   158 CHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKD-TVYTDFDGTRVYSPPEWIRYH 216
          |||||||||||||| :|| |||||||||||||| :| :|
Db   139 CHSHHIVHRDLKTENLLLDANM-NIKLADFGFGNFYKSGGEPLSTWCGSPPYAAPEVFEGK 197

Qy   217 RYHGRSAAVWSLGILLYDMVCGDIPFEHD------EEIIRGQVFFRQRVSSECQHLIRWC 270
          | |||||||||||||||:||| |:| :||
Db   198 EYEGPHLDIWSLGVVLVYVLVCGSLPFDGNLPFDGNPTLRQRVLEGRFRIPYFMSEDCSTLIRRM 257

Qy   271 LALRPSDRPTFEEIQNHPWMQ-DVLLPQE 298
          |:||||||||:|||||||| | :||
Db   258 LVDPTKRITISQIKQHKWMQADPSLRQQ 286

RESULT 14
JC1446
serine/threonine-specific protein kinase (EC 2.7.1.-) AK21 - Arabidopsis thaliana
N;Alternate names: protein kinase SNF1 homolog
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Oct-2004

C;Accession: JC1446; S58266; S66334
R;LeGuen, L.; Thomas, M.; Bianchi, M.; Halford, N.G.; Kreis, M.
Gene 120, 249-254, 1992
A;Title: Structure and expression of a gene from Arabidopsis thaliana encoding a protein
A;Reference number: JC1446; MUID:93013041; PMID:1339373
A;Accession: JC1446
A;Molecule type: DNA
A;Residues: 1-512 <LEG>
A;Cross-references: UNIPROT:Q38997; UNIPARC:UPI000012DE43; GB:M93023; NID:g166599; PIDN:
R;Thuemmler, F.; Kirchner, M.; Teuber, R.; Dittrich, P.
submitted to the EMBL Data Library, May 1995
A;Description: Differential accumulation of the transcripts of 22 novel protein kinase g
A;Reference number: S58256
A;Accession: S58266
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 144-198 <THU>
A;Cross-references: UNIPARC:UPI00000009DEE0; EMBL:X86966; NID:g928909; PIDN:CAA60529.1; PI
R;Thuemmler, F.; Kirchner, M.; Teuber, R.; Dittrich, P.
Plant Mol. Biol. 29, 551-565, 1995
A;Title: Differential accumulation of the transcripts of 22 novel protein kinase genes i
A;Reference number: S66314; MUID:96123333; PMID:8534852
A;Accession: S66334
A;Molecule type: DNA
A;Residues: 144-198 <TH2>
A;Cross-references: UNIPARC:UPI00000009DEE0; EMBL:X86966; NID:g928909; PIDN:CAA60529.1; PI
C;Comment: This enzyme plays an important role in a signal transduction cascade regulati
C;Genetics:
A;Gene: AKin10; AK21
A;Introns: 64/1; 125/3; 186/3; 230/3; 292/3; 322/3; 350/3; 396/3; 475/3
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
C;Superfamily: SNF1-related protein kinase; protein kinase homology
C;Keywords: ATP; magnesium; phosphotransferase; serine/threonine-specific protein kinase
F;17-271/Domain: protein kinase homology <KIN>
F;25-33/Region: protein kinase ATP-binding motif
F;48,67,142,144/Active site: Lys, Glu, Asp, Lys #status predicted
F;147,151/Binding site: magnesium (Asn, Asp) #status predicted

Query Match   21.6%;   Score 360; DB 1; Length 512;
Best Local Similarity 33.6%;   Pred. No. 2.6e-11;
Matches 90;   Conservative 51;   Mismatches 111;   Indels 16;   Gaps   8;

Qy   32 EPLESQYQVGPLLGSGGFGSVYSGIRVSDNLPVAIKHVEKDRISDWGELPNGTRVPMEVV 91
          |:|| :|||||||| ||
Db   13 ESILPNYKLGRTLGISGFGRVKIAEHALTGHKVAIKILNRRKIKN--MEMEEKVRREIK 69

Qy   92 LLKKVSSGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELARSFFWQV 151
          | |:| ||||| :
Db   70 ILRLFM--HPHIIRLYEVIETPTDIYLVMEYVNS-GELFDYIVEKGRLQEDEARNFFQQI 126

Qy   152 LEAVRHCHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVYTDFD-GTRVYSPP 210
          ||||||||||||||||| | :|| |||||||||||||
Db   127 ISGVEYCHRNMVVHRDLKPENLLLD-SKCNVKIADFGLSNIMRDGHFLKTSCGSPNYAAP 185

Qy   211 EWIRYHRYHGRSAAVWSLGILLYDMVCGDIPFEHDEEI------IRGQVF-FRQRVSSEC 263
          || | |::|||||||||||:||| |:|
Db   186 EVISGKLYAGPEVDVWSCGVILYALLCGTLPFD-DENIPNLFKKIKGGIYTLPSHLSPGA 244

Qy   264 QHLIRWCLALRPSDRPTFEEIQNHPWMQ 291
          |||| ||||||||||||||:||||||
Db   245 RDLIPRMLVVDPMKRVTIPEIRQHPWFQ 272

RESULT 15
A56009
serine/threonine-specific protein kinase (EC 2.7.1.-) NPK5 - common tobacco
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 05-Oct-2004
C;Accession: A56009
R;Muranaka, T.; Banno, H.; Machida, Y.
Mol. Cell. Biol. 14, 2958-2965, 1994
A;Title: Characterization of tobacco protein kinase NPK5, a homolog of Saccharomyces cei

tase of Saccharomyces cerevisiae.
A;Reference number: A56009; MUID:94217693; PMID:8164654
A;Accession: A56009
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-511 <MUR>
A;Cross-references: UNIPROT:Q40544; UNIPARC:UPI00000AAD0C; GB:D26602; NID:g496384; PIDN:
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
C;Superfamily: SNF1-related protein kinase; protein kinase homology
C;Keywords: ATP; magnesium; phosphotransferase; serine/threonine-specific protein kinase
F;17-271/Domain: protein kinase homology <KIN>
F;25-33/Region: protein kinase ATP-binding motif
F;48,67,142,144/Active site: Lys, Glu, Asp, Lys #status predicted
F;147,151/Binding site: magnesium (Asn, Asp) #status predicted

```
Query Match      21.5%;     Score 359; DB 1;    Length 511;
Best Local Similarity   31.7%;     Pred. No. 2.9e-11;
Matches   86;  Conservative   54;  Mismatches  117;   Indels   14;   Gaps    6;

Qy      28  GKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSDNLPVAIKHVEKDRISDWGELPNGTRVP  87
                :||:||| ||  ||||      |||:|:  :|:|| : :|:  :
Db       9  GSSVESFLRNYKLGKTLGIGSFGKVKIAEHTLTGHKVAVKILNRRKIKN---MEMEEKVR  65

Qy      88  MEVVLLKKVSSGFSGVIRLLDWFERPDSFVLILERPEPVQDLFPDFITERGALQEELARSF  147
                |:.:|:|          :||||   : :    :||| ||:| |||:|||
Db      66  REIKILRLFM--HPHIIRLYEVVETPSDIYVVMEYVKS-GELFDYIVEKGRLQEDEARKF  122

Qy     148  FWQVLEAVRHCHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVYTDFD-GTRV  206
                | |: |  :||| ||:|||| |:|:|: :| : :||        |:||| :|  :
Db     123  FQQIISGVEYCHRNMVVHRDLKPENLLLD-SKWNVKIADFGLSNIMRDGHFLKTSCGSPN  181

Qy     207  YSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDIPFEHD------EEIIRGQVFPRQRVS  260
                |: :||||          |||:|| ::||:|||:: :|:|  |:  :|
Db     182  YAAPEVISGKLYAGPEVDVWSCGVILYALLCGTLPFDDENIPNLFKKIKGGMISLPSHLS  241

Qy     261  SECQHLIRWCLALRPSDRPTFEEIQNHPWMQ  291
                : ||||       :|: ||| :||
Db     242  AGARDLIPRMLIVDPMKRMTIPEIRMHPWFQ  272
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Search completed: April 21, 2006, 12:59:19
Job time : 42 secs

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                    GenCore version 5.1.7
          Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on:   April 21, 2006, 12:50:45 ; Search time 189 Seconds
                                     (without alignments)
                                     727.648 Million cell updates/sec

Title:         US-10-664-421-1
Perfect score: 1670
Sequence: 1 MLLSKINSLAHLRAAPCNDL..........LLPQETAEIHLHSLSPGPSK 313

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched:  2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters:        2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   A_Geneseq_21:*
         1:  geneseqp1980s:*
         2:  geneseqp1990s:*
         3:  geneseqp2000s:*
         4:  geneseqp2001s:*
         5:  geneseqp2002s:*
         6:  geneseqp2003as:*
         7:  geneseqp2003bs:*
         8:  geneseqp2004s:*
         9:  geneseqp2005s:*

                              SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
```

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	1670	100.0	313	5	ABP54943	Abp54943 Human Pim
2	1670	100.0	313	5	ABG33017	Abg33017 Human pro
3	1670	100.0	313	6	AAO19788	Aao19788 Human PIM
4	1670	100.0	313	7	ABU61613	Abu61613 Human PIM
5	1670	100.0	313	7	ABR62939	Abr62939 Human ser
6	1670	100.0	313	7	ADE55368	Ade55368 Human Pro
7	1670	100.0	313	7	ADF45083	Adf45083 Human kin
8	1670	100.0	313	8	ADO19690	Ado19690 Human PRO
9	1670	100.0	313	8	ADR88370	Adr88370 Human PIM
10	1670	100.0	313	8	ADP24227	Adp24227 PRO polyp
11	1670	100.0	313	8	ADT07365	Adt07365 Human pro
12	1670	100.0	313	8	ADT14636	Adt14636 human Pim
13	1670	100.0	313	9	ADY86782	Ady86782 Human Pim
14	1670	100.0	313	9	AEA89424	Aea89424 Human Pim
15	1670	100.0	313	9	AEB96037	Aeb96037 Human PIM
16	1657	99.2	313	2	AAW08139	Aaw08139 Human cyt
17	1657	99.2	313	3	AAY87959	Aay87959 Human CR7
18	1657	99.2	313	8	ADI57202	Adi57202 Human PIM
19	1657	99.2	313	8	ADN03170	Adn03170 Human PIM
20	1657	99.2	313	9	ADY95580	Ady95580 Catalytic
21	1636	98.0	313	5	ABG33016	Abg33016 Rat prote
22	1636	98.0	313	6	AAO19789	Aao19789 Rat PIM1
23	1636	98.0	313	7	ABR62938	Abr62938 Rat serin
24	1636	98.0	313	9	AEB96039	Aeb96039 Norway ra
25	1582	94.7	313	5	ABG33015	Abg33015 Mouse pro
26	1582	94.7	313	6	AAO19790	Aao19790 Murine PI
27	1582	94.7	313	7	ABR62940	Abr62940 Mouse ser
28	1582	94.7	313	8	ADN97347	Adn97347 Murine Pi
29	1582	94.7	313	8	ADR88371	Adr88371 Mus muscu
30	1582	94.7	313	9	AEA19261	Aea19261 Mouse Pim
31	1582	94.4	313	9	AEB96041	Aeb96041 House mou
32	1576	94.4	313	9	AEA19263	Aea19263 Mouse Pim
33	1362	81.6	253	8	ADI57241	Adi57241 PIM1 domi
34	1296.5	77.6	257	8	AAY43942	Aay43942 Rat prote
35	1294.5	77.5	254	8	ADK71853	Adk71853 Human kin
36	1255	75.1	233	8	ADT07367	Adt07367 Human pro
37	1140	68.3	323	8	ADR88376	Adr88376 Colurnix
38	1135	68.0	326	2	AAY06886	Aay06886 HWHJ20 p
39	1135	68.0	374	8	ADX91611	Adx91611 Plant ful
40	1133	67.8	326	4	AAB29788	Aab29788 Human ser
41	1133	67.8	326	5	AAE23834	Aae23834 Human HKI
42	1133	67.8	326	5	ABG33011	Abg33011 Human ser
43	1133	67.8	326	6	ABR62932	Abr62932 Human pro
44	1133	67.8	326	7	ADJ96625	Adj96625 Human cal
45	1133	67.8	326	8	ADL97960	Adl97960 Human PIM

ALIGNMENTS

```
RESULT 1
ABP54943
ID   ABP54943 standard; protein; 313 AA.
XX
AC   ABP54943;
XX
DT   13-JAN-2003  (first entry)
XX
DE   Human Pim1.
XX
KW   Pim1; tyrosine threonine kinase; TTK; protein kinase; enzyme;
KW   mitotic checkpoint; colon cancer; breast cancer; tumour; cytostatic;
KW   human; gene therapy.
XX
OS   Homo sapiens.
XX
PN   WO200268444-A1.
XX
PD   06-SEP-2002.
XX
PF   21-FEB-2002; 2002WO-US005278.
XX
PR   21-FEB-2001; 2001US-0271254P.
XX
PA   (CHIR ) CHIRON CORP.
XX
PI   Reinhard C,  Jefferson AB,  Chan VW;
XX
DR   WPI; 2002-698650/75.
DR   N-PSDB; ABV73989.
XX
PT   Reducing growth of cancer cells comprises reducing Tyrosine Threonine
PT   Kinase (TTK) activity, useful in diagnosing and treating disorders with
PT   abnormal expression levels and activity of TTK, such as lung, colon,
PT   prostate and ovarian cancer.
XX
PS   Disclosure; Page 80-81; 113pp; English.
XX
CC   The present sequence is the protein sequence of human Pim1, a protein
CC   related to tyrosine threonine kinase (TTK, see ABP54938). TTK
CC   polynucleotides and polypeptides of the invention encompass
CC   polynucleotides and polypeptides having sequence similarity or sequence
CC   identity to human TTK and other genes and gene products related to TTK,
CC   such as Pim1. The invention is based on the finding that TTK is
CC   differentially expressed in various forms of cancer. It provides methods
CC   for the identification of cancerous cells, especially breast cancer and
CC   colon cancer cells, by detection of expression levels of TTK, as well as
```

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CC   diagnostic, prognostic and therapeutic methods. These methods can be used
CC   as the basis of rational therapy. Assays for identifying molecules that
CC   modulate the activity of these genes in cancers, as well as methods of
CC   inhibiting tumour growth by inhibiting the activity of TTK are also
CC   provided
XX
SQ   Sequence 313 AA;

Query Match             100.0%;  Score 1670;  DB 5;  Length 313;
Best Local Similarity   100.0%;  Pred. No. 1.4e-154;
Matches  313;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy          1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy         61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy        121 ERPEPVQDLFDFITERGAIQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ERPEPVQDLFDFITERGAIQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy        181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy        241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy        301 EIHLHSLSPGPSK 313
              |||||||||||||
Db        301 EIHLHSLSPGPSK 313

RESULT 2
ABG33017
ID   ABG33017 standard; protein; 313 AA.
XX
AC   ABG33017;
XX
DT   20-DEC-2002  (first entry)
XX
DE   Human protein kinase phosphorylation site.
XX
KW   HKID-1; serine/threonine kinase; cellular proliferative disorder;
KW   differentiative disorder; cancer; haematopoietic neoplastic disorder;
KW   Acute promyeloid leukaemia; APML; Chronic myelogenous leukaemia; CML;
KW   Waldenstrom's macroglobulinaemia; WM; human.
XX
OS   Homo sapiens.
XX
PN   US2002115120-A1.
XX
PD   22-AUG-2002.
XX
PF   04-OCT-2001; 2001US-00971791.
XX
PR   26-JAN-1999;  99US-00237543.
PR   23-AUG-2000; 2000US-00644450.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Kapeller-Libermann R, Rudolph-Owen LA, Macbeth K;
XX
DR   WPI; 2002-712471/77.
XX
PT   Modulating levels or activity of HKID-1 polypeptides, a member of
PT   serine/threonine kinase superfamily, for treating cancer, by contacting
PT   cell expressing the polypeptide with a modulator of the polypeptide.
XX
```

```
PS   Example 3; Page 40-41; 48pp; English.
XX
CC   The invention describes a method of modulating the level or activity of
CC   human HKID-1 polypeptide, a member of serine/threonine kinase
CC   superfamily. The method involves contacting a cell expressing the
CC   polypeptide or nucleic acid with an agent to modulate the level or
CC   activity of polypeptide, or level of nucleic acid molecule. The method is
CC   useful for modulating the level or activity of HKID-1 polypeptide or
CC   polynucleotide in a subject having or predisposed to having a disorder
CC   involving cancer. Modulating HKID-1 expression or activity is useful for
CC   therapeutic purposes, for treating cellular proliferative and/or
CC   differentiative disorders including cancer or haematopoietic neoplastic
CC   disorders e.g. Acute promyeloid leukaemia (APML), Chronic myelogenous
CC   leukaemia (CML) and Waldenstrom's macroglobulinaemia (WM). This is the
CC   amino acid sequence of a human protein kinase phosphorylation site
XX
SQ   Sequence 313 AA;

Query Match             100.0%;  Score 1670;  DB 5;  Length 313;
Best Local Similarity   100.0%;  Pred. No. 1.4e-154;
Matches  313;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy          1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy         61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy        121 ERPEPVQDLFDFITERGAIQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ERPEPVQDLFDFITERGAIQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy        181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy        241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy        301 EIHLHSLSPGPSK 313
              |||||||||||||
Db        301 EIHLHSLSPGPSK 313

RESULT 3
AAO19788
ID   AAO19788 standard; protein; 313 AA.
XX
AC   AAO19788;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Human PIM1 kinase.
XX
KW   Human; PIM1 kinase; PIM3 kinase; pain; analgesic.
XX
OS   Homo sapiens.
XX
PN   WO200293173-A2.
XX
PD   21-NOV-2002.
XX
PF   13-MAY-2002; 2002WO-EP005234.
XX
PR   11-MAY-2001; 2001DE-01023055.
XX
PA   (CHEF ) GRUENENTHAL GMBH.
XX
PI   Weihe E, Schaefer MK;
XX
```

```
DR   WPI; 2003-120715/11.
DR   N-PSDB; ABZ69186.
XX
PT   Method for identifying analgesics, useful particularly for treating
PT   chronic pain, by screening compounds for interaction with PIM-1 or -3
PT   kinase, or related compounds.
XX
PS   Claim 1; Fig 1B; 97pp; German.
XX
CC   The present invention relates to a method of identifying pain-regulating
CC   compounds, involving screening candidate compounds for interaction with
CC   PIM1 or PIM3 kinase. PIM1 and PIM3 proteins and coding sequences are
CC   useful for treating chronic pain, particularly of neuropathic or
CC   inflammatory origin (e.g. where associated with diabetes, cancer, AIDS or
CC   neurodegenerative diseases). The present sequence is human PIM1 kinase
XX
SQ   Sequence 313 AA;

Query Match       100.0%;  Score 1670;  DB 6;  Length 313;
Best Local Similarity  100.0%;  Pred. No. 1.4e-154;
Matches   313;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy    1  MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD  60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD  60

Qy   61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy  121  ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy  181  ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy  241  PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241  PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy  301  EIHLHSLSPGPSK 313
         |||||||||||||
Db  301  EIHLHSLSPGPSK 313

RESULT 4
ABU61613
ID   ABU61613 standard; protein; 313 AA.
XX
AC   ABU61613;
XX
DT   11-AUG-2003 (first entry)
XX
DE   Human PIM1 protein.
XX
KW   Human; tyrosine threonine kinase; TTK; cancer; cytostatic;
KW   mitotic checkpoint gene; PIM1.
XX
OS   Homo sapiens.
XX
PN   US2003045491-A1.
XX
PD   06-MAR-2003.
XX
PF   21-FEB-2002; 2002US-00081119.
PR   23-FEB-2001; 2001US-0289813P.
XX
PA   (REIN/) REINHARD C.
PA   (JEFF/) JEFFERSON A B.
PA   (CHAN/) CHAN V W.
```

```
XX
PI   Reinhard C, Jefferson AB, Chan VW;
XX
DR   WPI; 2003-455566/43.
DR   N-PSDB; ACA62265.
XX
PT   Detecting cancer in a subject, by comparing expression levels of tyrosine
PT   threonine kinase polypeptide or polynucleotide in a subject cell and a
PT   normal cell, where an increase in the expression level in the test cell
PT   is indicative of cancer.
XX
PS   Disclosure; Page 34-35; 79pp; English.
XX
CC   The invention relates to detecting cancer (other than ovarian cancer) in
CC   a subject, comprising comparing the expression levels of tyrosine
CC   threonine kinase (TTK, a mitotic checkpoint gene) polypeptide or
CC   polynucleotide in a test cell obtained from the subject and in a normal
CC   non-cancer cell, where an increase in the expression level of TTK protein
CC   or nucleic acid in the test cell compared to that in the normal cell,
CC   indicates the presence of cancer other than ovarian cancer. Also included
CC   are reducing growth of a cancerous cell (by contacting a cancerous cell
CC   with an amount of an agent effective to reduce TTK polypeptide activity
CC   in the cell), an assay for identifying a candidate agent that reduces
CC   growth of a cancerous cell (comprising: (i) detecting the activity of a
CC   TTK polypeptide in the presence of a candidate agent; and (ii) comparing
CC   the activity of TTK polypeptide in the presence of a candidate agent
CC   relative to TTK polypeptide activity in the absence of the candidate
CC   agent), identifying an agent that reduces TTK activity (comprising: (i)
CC   contacting a cancerous cell displaying elevated expression of a TTK-
CC   encoding polynucleotide with a candidate agent; and (ii) determining the
CC   effect of the candidate agent on TTK polypeptide activity) and assessing
CC   the prognosis of a cancerous disease other than ovarian cancer in a
CC   subject (comprising: (i) detecting expression of TTK -encoding
CC   polynucleotide in a test cancer cell of a subject; and (ii) comparing a
CC   level of expression of TTK-encoding polynucleotide in the test cancer
CC   cell with a level of expression of the polynucleotide in a control non-
CC   cancer cell, where the level of expression of TTK in the test cancer cell
CC   relative to the level of expression in the control non-cancer cell is
CC   indicative of the prognosis of the cancerous disease). The methods are
CC   useful for detecting cancer (other than ovarian cancer) in a subject,
CC   reducing growth of cancerous cells, identifying a candidate agent that
CC   reduces growth of a cancerous cell, identifying an agent that reduces TTK
CC   activity and assessing the prognosis of a cancerous disease other than
CC   ovarian cancer. The methods are also useful for determining the ability
CC   of a subject to respond to a particular therapy e.g. as a basis of
CC   rational therapy. The present sequence represents a closely related
CC   protein to human TTK, in this case human PIM1 (not defined)
XX
SQ   Sequence 313 AA;

Query Match       100.0%;  Score 1670;  DB 7;  Length 313;
Best Local Similarity  100.0%;  Pred. No. 1.4e-154;
Matches   313;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy    1  MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD  60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD  60

Qy   61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy  121  ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy  181  ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy  241  PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241  PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
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```
Qy    181  ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI  240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI  240

Qy    241  PFEHDEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA  300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  PFEHDEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA  300

Qy    301  EIHLHSLSPGPSK  313
                |||||||||||||
Db    301  EIHLHSLSPGPSK  313


RESULT 5
ABR62939
ID  ABR62939 standard; protein; 313 AA.
XX
AC  ABR62939;
XX
DT  04-DEC-2003  (first entry)
XX
DE  Human serine/threonine protein kinase PIM-1.
XX
KW  Human; PIM-1; protein kinase; enzyme.
XX
OS  Homo sapiens.
XX
PN  WO2003060130-A2.
XX
PD  24-JUL-2003.
XX
PF  20-JAN-2003; 2003WO-EP000492.
XX
PR  19-JAN-2002; 2002EP-00001401.
XX
PA  (AVET ) AVENTIS PHARMA DEUT GMBH.
XX
PI  Korn M, Mueller G, Schneider R, Tschank G;
XX
DR  WPI; 2003-598536/56.
XX
PT  New human or murine PIM-3 DNAs or polypeptides, useful for as a screening
PT  agent for identifying anti-type 2 diabetes mellitus drugs, or for
PT  treating insulin resistance or type 2 diabetes mellitus.
XX
PS  Example 2; Page 40; 40pp; English.
XX
CC  The present sequence is the protein sequence of the human
CC  serine/threonine protein kinase and proto-oncogene, PIM-1. PIM-1 proteins
CC  are the paralogues of novel human and murine PIM-3 proteins (see ABR62932
CC  and ABR62913) of the invention, which are therefore expected to be
CC  involved in cancer and cell growth regulation. PIM-3 is also involved in
CC  the development of insulin resistance and type 2 diabetes mellitus. The
CC  invention relates to the use of PIM-3 nucleic acids and proteins in:
CC  screening assays for compounds that modulate insulin resistance or type 2
CC  diabetes mellitus; detection assays for detecting insulin resistance or
CC  type 2 diabetes mellitus (e.g. chromosomal mapping, tissue typing,
CC  forensic biology); predictive medicine (e.g. diagnostic or prognostic
CC  assays, monitoring clinical trials, pharmacogenomics); and for the
CC  preparing a medicament for the treatment of insulin resistance or type 2
CC  diabetes mellitus
XX
SQ  Sequence 313 AA;

Query Match           100.0%;  Score 1670;  DB 7;  Length 313;
Best Local Similarity 100.0%;  Pred. No. 1.4e-154;
Matches  313;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy     1  MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD  60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1  MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD  60

Qy    61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL  120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL  120

Qy   121  ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG  180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG  180


RESULT 6
ADE55368
ID  ADE55368 standard; protein; 313 AA.
XX
AC  ADE55368;
XX
DT  29-JAN-2004  (first entry)
XX
DE  Human Protein AAA60089, SEQ ID NO 1183.
XX
KW  Human; pain; neuronal tissue; gene therapy;
KW  spinal segmental nerve injury; chronic constriction injury; CCI;
KW  spared nerve injury; SNI; Chung.
XX
OS  Homo sapiens.
XX
PN  WO2003016475-A2.
XX
PD  27-FEB-2003.
XX
PF  14-AUG-2002; 2002WO-US025765.
XX
PR  14-AUG-2001; 2001US-0312147P.
PR  01-NOV-2001; 2001US-0346382P.
PR  26-NOV-2001; 2001US-0333347P.
XX
PA  (GEHO ) GEN HOSPITAL CORP.
PA  (FARB ) BAYER AG.
XX
PI  Woolf C, D'urso D, Befort K, Costigan M;
XX
DR  WPI; 2003-268312/26.
DR  GENBANK; AAA60089.
XX
PT  New composition comprising two or more isolated polypeptides, useful for
PT  preparing a medicament for treating pain in an animal.
XX
PS  Claim 1; Page 1017pp; English.
XX
CC  The invention discloses a composition comprising two or more isolated rat
CC  or human polynucleotides or a polynucleotide which represents a fragment,
CC  derivative or allelic variation of the nucleic acid sequence. Also
CC  claimed are a vector comprising the novel polynucleotide, a host cell
CC  comprising the vector, a method for identifying a nucleotide sequence
CC  which is differentially regulated in an animal subjected to pain and a
CC  kit to perform the method, an array, a method for identifying an agent
CC  that increases or decreases the expression of the polynucleotide sequence
CC  that is differentially expressed in neuronal tissue of a first animal
CC  subjected to pain, a method for identifying a compound which regulates
CC  the expression of a polynucleotide sequence which is differentially
CC  expressed in an animal subjected to pain, a method for identifying a
CC  compound that regulates the activity of one or more of the
CC  polynucleotides, a method for producing a pharmaceutical composition, a
CC  method for identifying a compound or small molecule that regulates the
CC  activity in an animal of one or more of the polypeptides given in the
CC  specification, a method for identifying a compound useful in treating
CC  pain and a pharmaceutical composition comprising the one or more
CC  polypeptides or their antibodies. The polynucleotide or the compound that
CC  modulates its activity is useful for preparing a medicament for treating
CC  pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
```

CC   injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC   therapy). The sequence presented is a human protein (shown in Table 2 of
CC   the specification) which is differentially expressed during pain. Note:
CC_   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic form directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 313 AA;

Query Match   100.0%; Score 1670; DB 7; Length 313;
Best Local Similarity   100.0%; Pred. No. 1.4e-154;
Matches 313; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy   241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy   301 EIHLHSLSPGPSK 313
          |||||||||||||
Db   301 EIHLHSLSPGPSK 313

RESULT 7
ADF45083
ID   ADF45083 standard; protein; 313 AA.
XX
AC   ADF45083;
XX
DT   12-FEB-2004 (first entry)
XX
DE   Human kinase PIM1.
XX
KW   Human; protein kinase; enzyme; inhibitor; PIM1.
XX
OS   Homo sapiens.
XX
PN   WO2003081210-A2.
XX
PD   02-OCT-2003.
XX
PF   20-MAR-2003; 2003WO-US008725.
PR   21-MAR-2002; 2002US-0366892P.
XX
PA   (SUNE-) SUNESIS PHARM INC.
XX
PI   Prescott JC, Braisted A;
XX
DR   WPI; 2003-865136/80.
XX
PT   Identifying ligand binding to inactive conformation of target protein
PT   kinase (T) comprises contacting the conformation modified (T) which
PT   contains reactive group at binding site, with ligands and detecting
PT   kinase-ligand conjugate formation.
XX
PS   Disclosure; SEQ ID NO 52; 260pp; English.
XX

CC   The present invention relates to a method for identifying a ligand (L),
CC   which binds to an inactive conformation of target protein kinase (T). The
CC   method involves contacting inactive conformation of (T), which contains
CC   or is modified to contain a reactive group at or near a binding site of
CC   interest, with one or more ligand candidates capable of covalently
CC   bonding to the reactive group thus forming a kinase-(L) conjugate (C).
CC   The method is useful for identifying protein kinase inhibitors that
CC   preferentially bind to inactive conformation of a target protein kinase.
CC   The present sequence is a protein kinase which may be modified via an
CC   amino acid substitution, for use in the method of the invention.
XX
SQ   Sequence 313 AA;

Query Match   100.0%; Score 1670; DB 7; Length 313;
Best Local Similarity   100.0%; Pred. No. 1.4e-154;
Matches 313; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy   241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy   301 EIHLHSLSPGPSK 313
          |||||||||||||
Db   301 EIHLHSLSPGPSK 313

RESULT 8
ADO19690
ID   ADO19690 standard; protein; 313 AA.
XX
AC   ADO19690;
XX
DT   12-AUG-2004 (first entry)
XX
DE   Human PRO polypeptide #308.
XX
KW   Human; PRO; immune related disorder; systemic lupus erythematosus;
KW   rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis;
KW   systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis;
KW   autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis;
KW   diabetes mellitus; renal disease; demyelinating disease;
KW   central nervous system; peripheral nervous system;
KW   demyelinating polyneuropathy; Guillain-Barre syndrome;
KW   chronic inflammatory demyelinating polyneuropathy.
XX
OS   Homo sapiens.
XX
PN   WO2004043361-A2.
XX
PD   27-MAY-2004.
XX
PF   06-NOV-2003; 2003WO-US035268.
XX
PR   08-NOV-2002; 2002US-0425235P.
XX
PA   (GETH) GENENTECH INC.
XX

```
PI  Fong S, Dennis K, Clark H, Chiu H, Schoenfeld J, Williams PM;
PI  Wood WI, Wu TD;
XX
DR  WPI; 2004-420067/39.
DR  N-PSDB; AD019689.
XX
PT  Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for
PT  treating an immune related disorder such as systemic lupus erythematosus,
PT  rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or
PT  spondyloarthropathy.
XX
PS  Claim 7; SEQ ID NO 616; 1731pp; English.
XX
CC  The invention relates to human PRO polypeptides and the polynucleotides
CC  encoding them. The polypeptides and polynucleotides are useful for
CC  treating and diagnosing immune related disorders in mammals. The immune
CC  related disorders include systemic lupus erythematosus, rheumatoid
CC  arthritis, osteoarthritis, juvenile chronic arthritis, systemic
CC  sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune
CC  haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes
CC  mellitus, immune-mediated renal disease, demyelinating diseases of the
CC  central or peripheral nervous system, demyelinating polyneuropathy,
CC  Guillain-Barre syndrome and chronic inflammatory demyelinating
CC  polyneuropathy. This sequence represents a human PRO polypeptide of the
CC  invention.
XX
SQ  Sequence 313 AA;

Query Match      100.0%;   Score 1670;  DB 8;  Length 313;
Best Local Similarity  100.0%;  Pred. No. 1.4e-154;
Matches  313;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1  MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD  60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD  60

Qy   61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL  120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL  120

Qy  121  ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG  180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG  180

Qy  181  ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYRYRHGRSAAVWSLGILLYDMVCGDI  240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYRYRHGRSAAVWSLGILLYDMVCGDI  240

Qy  241  PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA  300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241  PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA  300

Qy  301  EIHLHSLSPGPSK  313
            |||||||||||||
Db  301  EIHLHSLSPGPSK  313

RESULT 9
ADR88370
ID   ADR88370 standard; protein; 313 AA.
XX
AC   ADR88370;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Human PIM 1 protein.
XX
KW   Molecular scaffold; nuclear hormone receptor; TNF receptor;
KW   G-protein coupled receptor; methyl transferase; ligase; PIM; human.
XX
OS   Homo sapiens.
XX
PN   US2004171062-A1.
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XX
PD   02-SEP-2004.
XX
PF   28-FEB-2003; 2003US-00377268.
XX
PR   28-FEB-2002; 2002US-0360651P.
PR   16-SEP-2002; 2002US-0411398P.
PR   20-SEP-2002; 2002US-0412341P.
PR   02-JAN-2003; 2003US-0437929P.
XX
PA   (PLEX-) PLEXXIKON INC.
XX
PI   Hirth K, Milburn MV;
XX
DR   WPI; 2004-642017/62.
XX
PT   Designing a ligand binding to a target molecule, comprises identifying as
PT   molecular scaffolds compounds binding to members of a molecular family,
PT   detecting orientation of scaffolds at a binding site of target, and
PT   synthesizing ligand.
XX
PS   Disclosure; SEQ ID NO 9; 186pp; English.
XX
CC   The present invention relates to a method of designing a ligand binding
CC   to a target molecule. The method involves identifying as molecular
CC   scaffolds compounds binding to members of a molecular family, detecting
CC   orientation of scaffolds at a binding site of target, and synthesising
CC   ligand. The invention is useful for designing drug products and for
CC   designing ligand binding to target molecules such as nuclear hormone
CC   receptors, TNF receptors, G-protein coupled receptors, methyl
CC   transferases, ligases, etc. The present sequence is the human PIM 1
CC   protein. This sequence is used to illustrate the method of invention.
XX
SQ   Sequence 313 AA;

Query Match      100.0%;   Score 1670;  DB 8;  Length 313;
Best Local Similarity  100.0%;  Pred. No. 1.4e-154;
Matches  313;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1  MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD  60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD  60

Qy   61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLKKVSSGFSGVIRLLDWFERPDSFVLIL  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLKKVSSGFSGVIRLLDWFERPDSFVLIL  120

Qy  121  ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG  180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG  180

Qy  181  ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYRYRHGRSAAVWSLGILLYDMVCGDI  240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYRYRHGRSAAVWSLGILLYDMVCGDI  240

Qy  241  PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA  300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241  PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA  300

Qy  301  EIHLHSLSPGPSK  313
            |||||||||||||
Db  301  EIHLHSLSPGPSK  313

RESULT 10
ADP24227
ID   ADP24227 standard; protein; 313 AA.
XX
AC   ADP24227;
XX
DT   18-NOV-2004  (first entry)
XX
DE   PRO polypeptide SEQ ID NO:1405.
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XX
KW   PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive;
KW   osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic;
KW_  antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.
XX
OS   Unidentified.
XX
PN   WO200041170-A2.
XX
PD   21-MAY-2004.
XX
PF   30-OCT-2003; 2003WO-US034312.
XX
PR   01-NOV-2002; 2002US-0423394P.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Clark H,  Schoenfeld J,  Van Lookeren M,  Williams PM,  Wood WI;
PI   Wu TD;
XX
DR   WPI; 2004-419628/39.
DR   N-PSDB; ADP24226.
XX
PT   New PRO polypeptides and polynucleotides, useful for treating e.g.
PT   erythematosus, rheumatoid arthritis, diabetes mellitus, immune-mediated
PT   renal disease, or demyelinating diseases of the central or peripheral
PT   nervous system.
XX
PS   Claim 7; SEQ ID NO 1405; 2940pp; English.
XX
CC   The invention relates to a novel isolated nucleic acid and the PRO
CC   polypeptide encoded by it. A protein of the invention has
CC   antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,
CC   osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic,
CC   antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide
CC   of the invention may have a use in gene therapy. The PRO polypeptide, its
CC   agonist, antagonist, or antibody that specifically binds to the
CC   polypeptide is useful for treating an immune related disorder such as
CC   systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
CC   juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
CC   idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
CC   vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
CC   thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
CC   disease, a demyelinating disease of the central or peripheral nervous
CC   system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
CC   a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
CC   disease, infectious or autoimmune chronic active hepatitis, primary
CC   biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
CC   inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
CC   disease, an autoimmune or immune-mediated skin disease, a bullous skin
CC   disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
CC   disease, asthma, allergic rhinitis, atopic dermatitis, food
CC   hypersensitivity, urticaria, an immunologic disease of the lung,
CC   eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
CC   pneumonitis, a transplantation associated disease, graft rejection or
CC   graft-versus-host disease. The present sequence represents a PRO protein
CC   of the invention.
XX
SQ   Sequence 313 AA;

Query Match             100.0%;  Score 1670;  DB 8;  Length 313;
Best Local Similarity   100.0%;  Pred. No. 1.4e-154;
Matches  313;  Conservative   0;  Mismatches  0;  Indels   0;  Gaps     0;

Qy          1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy         61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy        121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
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Db        121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy        181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Db        181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy        241 PFEHDEEIIRGQVFPRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 PFEHDEEIIRGQVFPRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy        301 EIHLHSLSPGPSK 313
              |||||||||||||
Db        301 EIHLHSLSPGPSK 313


RESULT 11
ADT07365
ID   ADT07365 standard; protein; 313 AA.
XX
AC   ADT07365;
XX
DT   13-JAN-2005  (first entry)
XX
DE   Human protein #1 associated to anticancer compound screening method.
XX
KW   Prophylactic-therapeutic agent; apoptosis inducing agent;
KW   anticancer agent; serine/threonine kinase Pim-1; cancer; solid tumour;
KW   human.
XX
OS   Homo sapiens.
XX
PN   WO200409158-A1.
XX
PD   21-OCT-2004.
XX
PF   05-APR-2004; 2004WO-JP004917.
PR   03-APR-2003; 2003US-0459644P.
XX
PA   (ONCO-) ONCOREX INC.
XX
PI   Kobayashi M,  Jian C;
XX
DR   WPI; 2004-748778/73.
DR   N-PSDB; ADT07366.
XX
PT   Screening for a prophylactic-therapeutic apoptosis inducing agent or
PT   enhancer of anticancer agent, comprises use of serine/threonine kinase
PT   Pim-1, its partial peptide or its salt.
XX
PS   Disclosure; SEQ ID NO 1; 93pp; Japanese.
XX
CC   The invention relates to a method of screening a prophylactic-therapeutic
CC   agent for an apoptosis inducing agent or an enhancer of an anticancer
CC   agent. The method involves the use of a serine/threonine kinase Pim-1,
CC   its partial peptide or its salt. Also disclosed is a kit for carrying out
CC   the method of the invention. The method is useful for screening a
CC   prophylactic-therapeutic agent for cancer. The method is also useful for
CC   prophylaxis and/or treatment of cancer, inducing apoptosis, treating a
CC   patient having a solid tumour that is resistant to an anticancer agent
CC   (induced by hypoxia), and for screening a substance that promotes or
CC   inhibits the activity of serine/threonine kinase Pim-1. The present
CC   sequence represents a human polypeptide relating to the present
CC   invention.
XX
SQ   Sequence 313 AA;

Query Match             100.0%;  Score 1670;  DB 8;  Length 313;
Best Local Similarity   100.0%;  Pred. No. 1.4e-154;
Matches  313;  Conservative   0;  Mismatches  0;  Indels   0;  Gaps     0;

Qy          1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
```

```
Db           |||||||||||||||||||||||||||||||||||||||||||||||||
Qy         1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
             |||||||||||||||||||||||||||||||||||||||||||||||||
Qy        61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
             |||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
Qy       121 ERREPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
             |||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 ERREPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
Qy       181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
             |||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
Qy       241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
             |||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
Qy       301 EIHLHSLSPGPSK 313
             |||||||||||||
Db       301 EIHLHSLSPGPSK 313
```

RESULT 12
ADT14636
ID   ADT14636 standard; protein; 313 AA.
XX
AC   ADT14636;
XX
DT   13-JAN-2005 (first entry)
XX
DE   human Pim-1 (oncogene-encoded serine/threonine kinase) protein.
XX
KW   crystallography; Pim-1; cancer; serine/threonine kinase; enzyme;
KW   protein co-ordinate data; protein structure.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   Domain   33..121
FT   /note = N-terminal domain
FT   Domain   44..52
FT   /note = Glycine-rich loop
FT   Domain   122..127
FT   /note = Hinge region
FT   Domain   128..305
FT   /note = C-terminal domain
FT   Modified-site 166
FT   /label= OTHER
FT   /note= "OTHER = Forms a salt bridge via linkage to
FT   Asp200"
FT   Domain   186..210
FT   /note = Activation loop
FT   Modified-site 200
FT   /label= OTHER
FT   /note= "OTHER = Forms a salt bridge via linkage to
FT   Arg166"
XX
PN   WO2004090106-A2.
XX
PD   21-OCT-2004.
XX
PF   01-APR-2004; 2004WO-US010345.
XX
PR   04-APR-2003; 2003US-0460843P.
PR   12-MAR-2004; 2004US-0552526P.
XX
PA   (VERT-) VERTEX PHARM INC.
XX
PI   Jacobs ML, Hare B, Swenson L;
XX
DR   WPI; 2004-757977/74.

XX
PT   Crystal useful for developing Pim-1 (oncogene-encoded serine/threonine
PT   kinase) inhibitors, comprises human Pim-1 protein, Pim-1 homologue, human
PT   Pim-1 protein complex, or Pim-1 homologue complex.
XX
PS   Claim 8; SEQ ID NO 2; 219pp; English.
XX
CC   The invention relates to a novel crystal comprising a human Pim-1
CC   (oncogene-encoded serine/threonine kinase) protein, a Pim-1 homologue, a
CC   human Pim-1 protein complex or a Pim-1 homologue complex. Pim-1 is
CC   primarily expressed in haemopoietic and germ cell lines and this
CC   expression is tightly regulated and induced by cytokines, mitogens and
CC   hormones. Human Pim-1 is associated with multiple cellular functions,
CC   such as proliferation, differentiation, apoptosis and tumourigenesis. The
CC   crystal of the invention relates particularly to the residues involved in
CC   the active site and binding sites of Pim-1. Such information may be
CC   useful for developing Pim-1 inhibitors that are useful as therapeutic
CC   agents in the treatment of cancer. The current sequence is that of the
CC   human Pim-1 (oncogene-encoded serine/threonine kinase) protein of the
CC   invention.
XX
SQ   Sequence 313 AA;

Query Match   100.0%; Score 1670; DB 8; Length 313;
Best Local Similarity   100.0%; Pred. No. 1.4e-154;
Matches 313; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy         1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
             |||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
Qy        61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
             |||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
Qy       121 ERREPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
             |||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 ERREPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
Qy       181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
             |||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
Qy       241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
             |||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
Qy       301 EIHLHSLSPGPSK 313
             |||||||||||||
Db       301 EIHLHSLSPGPSK 313
```

RESULT 13
ADY86782
ID   ADY86782 standard; protein; 313 AA.
XX
AC   ADY86782;
XX
DT   02-JUN-2005 (first entry)
XX
DE   Human Pim1 protein, SEQ ID NO: 18.
XX
KW   Prognosis; cancer; cytostatic; neoplasm; tyrosine threonine kinase; TTK;
KW   Pim1.
XX
OS   Homo sapiens.
XX
PN   US2005063974-A1.
XX
PD   24-MAR-2005.
XX
PF   27-SEP-2004; 2004US-00951477.
XX

```
PR   21-FEB-2001; 2001US-0271254P.
PR   23-FEB-2001; 2001US-0289813P.
PR   21-FEB-2002; 2002US-00081119.
XX
PA   (REIN/) REINHARD C.
PA   (JEFF/) JEFFERSON A B.
PA   (CHAN/) CHAN V W.
XX
PA-  Reinhard C, Jefferson AB,  Chan VW;
XX
DR   WPI; 2005-241248/25.
DR   N-PSDB; ADY86781.
XX
PT   Assessment of prognosis of a cancerous disease other than ovarian cancer
PT   comprises detection and comparison of expression of a tyrosine threonine
PT   kinase-encoding polynucleotide in a test cancer cell with a control non-
PT   cancer cell.
XX
PS   Disclosure; SEQ ID NO 18; 78pp; English.
XX
CC   The invention relates to a method for assessing the prognosis of a
CC   cancerous disease other than ovarian cancer which involves detection and
CC   comparison of expression of a tyrosine threonine kinase (TTK)-encoding
CC   polynucleotide in a test cancer cell with a control non-cancer cell. The
CC   method is useful to assess the prognosis of a cancerous disease other
CC   than ovarian cancer. It is useful to identify cancerous cells and to
CC   determine the ability of a subject to respond to a particular therapy
CC   e.g. as the basis of rational therapy. The present sequence is the TTK
CC   related human Pim1 protein.
XX
SQ   Sequence 313 AA;

Query Match             100.0%;    Score 1670;  DB 9;  Length 313;
Best Local Similarity   100.0%;    Pred. No. 1.4e-154;
Matches   313;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy    1  MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy   61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy  121  ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy  181  ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy  241  PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241  PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy  301  EIHLHSLSPGPSK 313
            |||||||||||||
Db  301  EIHLHSLSPGPSK 313

RESULT 14
AEA89424
ID   AEA89424 standard; protein; 313 AA.
XX
AC   AEA89424;
XX
DT   25-AUG-2005  (first entry)
XX
DE   Human Pim1 protein, SEQ ID NO: 18.
XX
KW   Drug screening; diagnosis; therapeutic; cancer; cytostatic; neoplasm;
KW   Pim1.
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XX
OS   Homo sapiens.
XX
PN   US2005130926-A1.
XX
PD   16-JUN-2005.
XX
PF   28-OCT-2004; 2004US-00977087.
XX
PR   04-NOV-1998;  98US-0107112P.
PR   06-JAN-1999;  99US-0114856P.
PR   14-MAY-1999;  99US-0134112P.
PR   26-JUL-1999;  99US-0145612P.
PR   13-AUG-1999;  99US-0149936P.
PR   03-NOV-1999;  99US-00433360.
PR   12-MAY-2000;  2000US-00570593.
PR   25-JUL-2000;  2000US-00626301.
PR   21-FEB-2001;  2001US-0271254P.
PR   21-FEB-2002;  2002US-00081119.
PR   06-FEB-2003;  2003US-00360848.
PR   30-OCT-2003;  2003US-00698959.
PR   22-JAN-2004;  2004US-00763692.
XX
PA   (CHIR ) CHIRON CORP.
XX
PI   Reinhard C,  Jefferson AB,  Chan VW,  Kaufmann J,  Xin H,  Kennedy GC;
PI   Harrowe G,  Khoja H,  Shyamala V;
XX
DR   WPI; 2005-457024/46.
DR   N-PSDB; AEA89423.
XX
PT   New isolated human HX2004-6 polypeptide or isolated VSHK-1 polypeptide,
PT   useful for diagnosing or treating cancer, where VSHK-1 is also used to
PT   identify a VSHK-1 receptor ligand.
XX
PS   Disclosure; SEQ ID NO 18; 206pp; English.
XX
CC   The invention relates to human HX2004-6 protein and a seven transmembrane
CC   receptor protein referred as VSHK-1 useful for diagnosing or treating
CC   cancer. The invention also relates to a method for reducing the growth of
CC   a cancerous cell. VSHK-1 is useful for identifying a VSHK-1 receptor
CC   ligand and to identify a substance which modulates its signal
CC   transduction activity. The HX2004-6 DNA is useful to detect the presence
CC   of HX2004-6 in a biological sample (e.g. ductal epithelial cells from
CC   tissue chosen from pancreas, colon and breast). The invention is useful
CC   for screening drugs for the treatment of cancer. The present sequence is
CC   the human Pim1 protein. This sequence is differentially expressed in
CC   cancer cells.
XX
SQ   Sequence 313 AA;

Query Match             100.0%;    Score 1670;  DB 9;  Length 313;
Best Local Similarity   100.0%;    Pred. No. 1.4e-154;
Matches   313;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy    1  MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy   61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy  121  ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy  181  ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy  241  PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db     241  PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA  300

Db     121  ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG  180

Qy     181  ELKLIDFGSGALLKDTVTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181  ELKLIDFGSGALLKDTVTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI  240

Qy     241  PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241  PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA  300

Qy     301  EIHLHSLSPGPSK  313
            |||||||||||||
Db     301  EIHLHSLSPGPSK  313
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Search completed: April 21, 2006, 12:54:03
Job time : 192 secs

```
RESULT 15
AEB96037
ID   AEB96037 standard; protein; 313 AA.
XX
AC   AEB96037;
XX
DT   20-OCT-2005  (first entry)
XX
DE   Human PIM-1 serine-threonine kinase protein.
XX
KW   micturition disorder; urinary dysfunction; uropathic; gene therapy;
KW   PIM-1 protein kinase; serine-threonine kinase; enzyme.
XX
OS   Homo sapiens.
XX
PN   DE102004004894-A1.
XX
PD   18-AUG-2005.
XX
PF   30-JAN-2004; 2004DE-10004894.
XX
PR   30-JAN-2004; 2004DE-10004894.
XX
PA   (CHEF ) GRUENENTHAL GMBH.
XX
PI   Christoph T;
XX
DR   WPI; 2005-556609/57.
DR   N-PSDB; AEB96036.
DR   REFSEQ; NP_002639.
XX
PT   Identifying substances that regulate PIM kinases, useful for treatment
PT   and diagnosis of urinary incontinence and the urge to urinate, and
PT   similar use of PIM proteins or nucleic acids.
XX
PS   Claim 1; Fig 1B; 37pp; German.
XX
CC   The invention relates to a novel method for identifying substances that
CC   regulate urinary incontinence and the urge to urinate. The method
CC   comprises incubating a test compound with a cell and/or cell preparation
CC   that has synthesized a specific protein of the PIM (proviral integration
CC   site) kinase family and measuring either binding of the test compound to
CC   the PIM kinase, or a functional parameter that is altered by the binding.
CC   The method of the invention demonstrates uropathic and gene therapy
CC   applications and may be useful for treatment and diagnosis of urinary
CC   incontinence and the urge to urinate. The method is based upon regulating
CC   the activity or expression of PIM kinases that are involved in bladder
CC   control. The current sequence is that of the human PIM-1 serine-threonine
CC   kinase protein of the invention.
XX
SQ   Sequence 313 AA;
```

Query Match   100.0%; Score 1670; DB 9; Length 313;
Best Local Similarity 100.0%; Pred. No. 1.4e-154;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy     1  MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD  60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1  MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD  60

Qy    61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL  120

Qy   121  ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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